1
A

```
2                                                   32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG
arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr

62                                                  92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC
ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser

122                                                 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA
trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala

182                                                 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser

242                                                 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302                                                 332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp

362                                                 392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

                Cadherin
422         |xxx cleavage xx|                       452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482                                                 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542                                                 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602                                                 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
```

FIG. 1
1 of 6

662 692

AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752

CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro

782 812

TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842 872

ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

Cadherin

|xx EC motif xx| 932

GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT
val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his

962 992

AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022 1052

TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082 1112

ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142 1172

ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val

1202 1232

GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu

1262 1292

ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322 1352

ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

FIG. 1
2 of 6

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1382                                                    1412
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
asp leu ser val leu gln leu asn arg leu leu asp l u l u tyr leu cys val ser cys

1442                                                    1472
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1502                                                    1532
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu

1562                                                    1592
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1622                                                    1652
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu

1682                                                    1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1742                                                    1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1802                                                    1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

1862                                                    1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1922                                                    1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1982                                                    2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2042                                                    2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro
```

FIG. 1
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2102                                                    2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162                                                    2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222                                                    2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282                                                    2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342                                                    2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402                |xxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxxxxxx
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

xxxxxxxxxxxxxxx|                                       2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522                                                    2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582                                                    2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642                                                    2672    |xxxxx ITAM xxxx|          |xxx
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

xx ITAM xxx|                                            2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762                                                    2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met
```

FIG. 1
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2822 |xxxxx ITAM xxxx| 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032|xxxxx ITAM xxxx|
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242 3272 |xxxxxxxxxxxxxxxxxxxxxx
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422 3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482 3512 |xxxxxxxxxxx
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

FIG. 1
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xxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602 3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro STP

3662 3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722 3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782 3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842 3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902 3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962 3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022 4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG

4082 4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142
CTC

FIG. 1
6 of 6

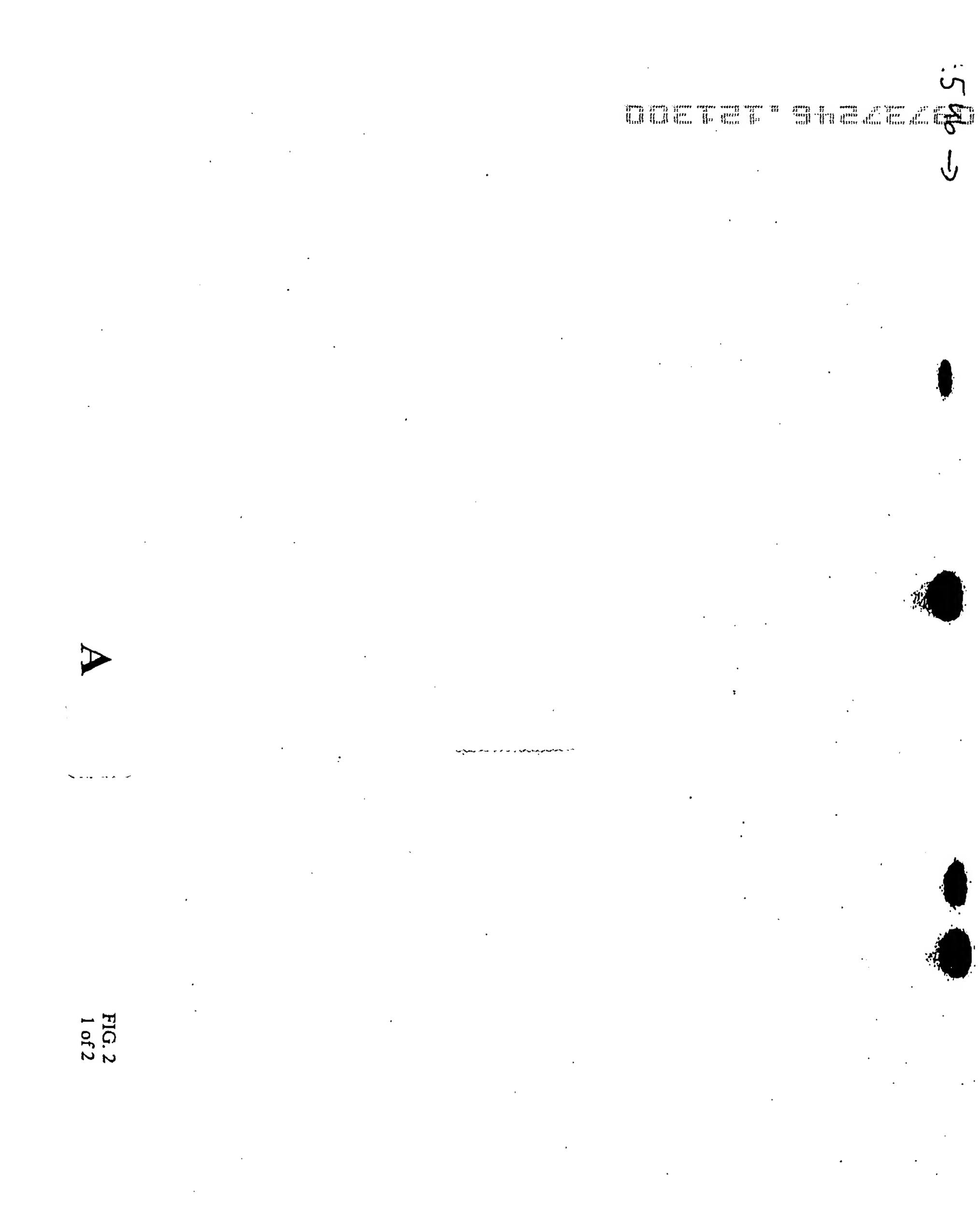
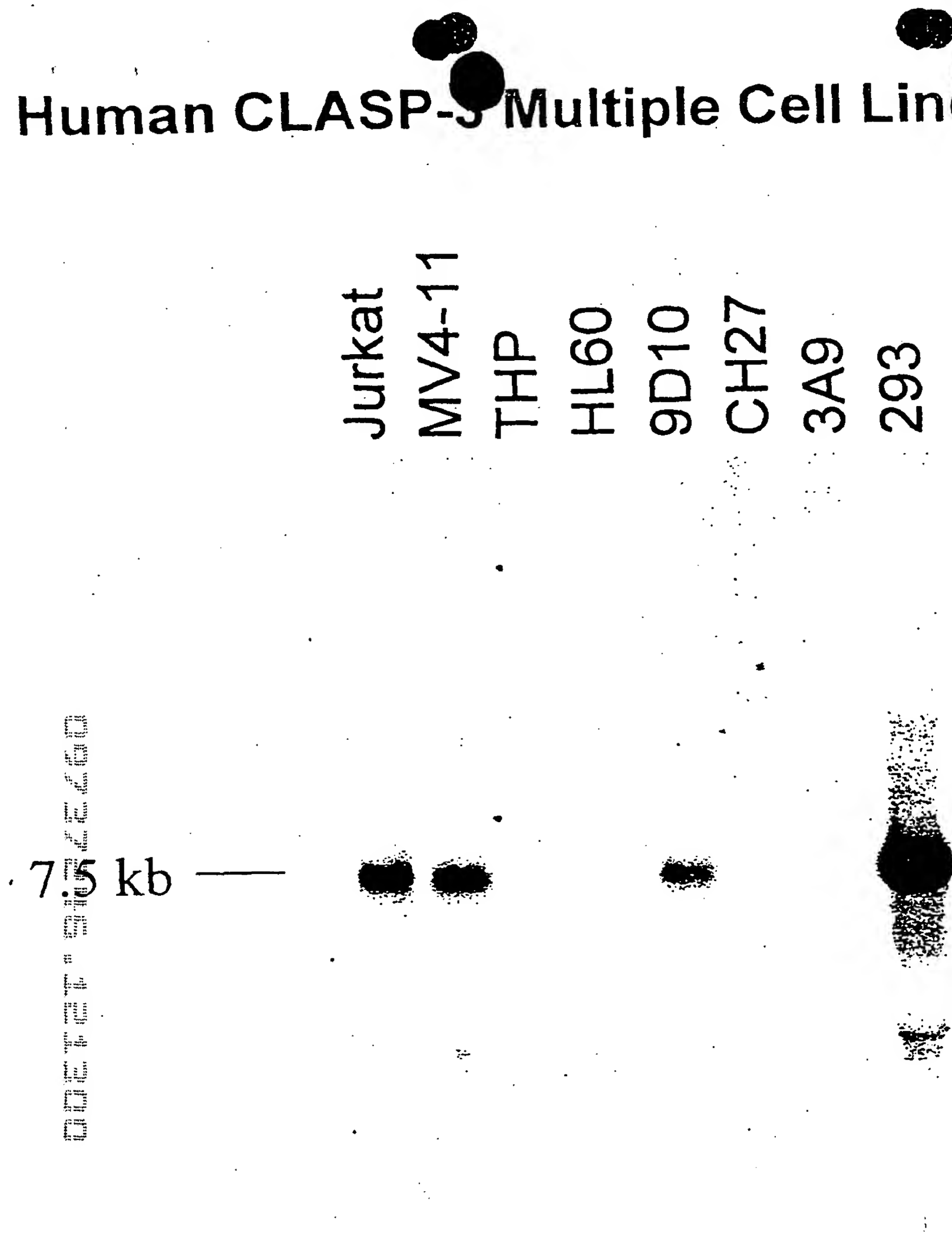


FIG. 2
1 of 2

Human CLASP-3 Multiple Cell Lines Northern



B

FIG. 2
2 of 2

```
HC2A    ------------------------------------------------------------
KIAA    ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ------------------------------------------------------------
KIAA    FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ----------------------------------------------------VLHHHQNPEFYDEIK
KIAA    KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ----------------------------------------GPGPARSTVSISLISNSARV
HC5     ------------------------------------------------------------

HC2A    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat     ------------------------------------------------------------
HC4     ----------------------MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1     ----------------------------MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3     NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5     ------------------------------------------------------------
```

A

FIG. 3
1 of 5

```
HC2A        IIHVVAQCHE LESHLRSYVKYAYKAEPYVASEYKTVHEELTK ILKPSADFLTSN
KIAA        IIHVVAQCH  ESHLRSYVKYAYKAEPYVASEYKTVHEELTR ILKPSADFLTSN
rat         ------------------------------------------------------
HC4         LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1         LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3         TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5         ------------------------------------------------------

                                          Cadherin
                                          Cleavage
HC2A        KLLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA        KLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat         ------------------------------------------------------------
HC4         KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1         HVLKHSWFFFAIILKSMAQHLIDTNKIQLPRPQRFPESYQNELDNLVMVLSDHVIWKYKD
HC3         SALQQAWFFFELMVKSMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK
HC5         ------------------------------------------------------------

HC2A        NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA        NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat         ------------------------------------------------------------
HC4         IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1         ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLCQYKFDFL
HC3         DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5         ------------------------------------------------------------

HC2A        RVVCNHEHYIPLNLPM-----PFGKGRIQR-----------YQDLQL----DYSLTDEF
KIAA        RVVCNHEHYIPLNLPM-----PFGKGRIQR-----------YQDLQL----DYSLTDEF
rat         ------------------------------------------------------------
HC4         QTICNHEHYIPLNLPM-----AFAKPKLQR-----------VQDSNL----EYSLSDEY
HC1         QEVCQHEHFIPLCLPIRSANIPDPLTPSES-----------TQELHASDMPEYSVTNEF
HC3         RIICSHEHYVTLNLPCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5         ---------------MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

                  Cadherin
                  EC motif
HC2A        CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA        CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat         ------------------------------------------------------------
HC4         CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1         CRKHFLIGLLLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3         RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAM
HC5         SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA

HC2A        LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA        LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat         ------------------------------------------------------------
HC4         LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1         LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
HC3         LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE----------SG---SMIS
HC5         LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE----------GA---GAIT
```

A

FIG. 3
2 of 5

```
HC2A        KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
KIAA'       KDLLGAISGI[redacted]YTTSTPNINSVRNADSRGSLISTDSGNSLPE[redacted]KSNSLDKHQQSS
rat         ----------[redacted]----------
HC4         TDKDTAYGSFQNG--------HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS
HC1         KDVLNSIAAFSS------IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3         QTVAMAIAGTSVPQ--------------------LTRPGSFLLTSTSGRQHT---------
HC5         QNVALAIAGNNFN---------------------LKTSG-IVLSSLPYKQYN---------

HC2A        TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA        TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat         ------------------------------------------------------------
HC4         STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1         ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3         ----------TFSAESSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLYLCV
HC5         ----------MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A        HQFQYMGKRYIARNQEGLG--PIVHDRKS----------------QTLPVSRNRTGMM
KIAA        HQFQYMGKRYIAR---------------------------------TGMM
rat         ------------------------------------------------------------
HC4         FHFRYMGKRNIARVHDAWLSKHFGIDRKS----------------QTMPALRNRSGVM
HC1         QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3         SCFEYKGKKVFERMNSLTFK--KSKDMRAK--------------LEEAILGSIGARQEMV
HC5         LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR--------------LEEALLRGEGARGEMM

HC2A        HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA        HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
rat         ------------------------------------------------------------
HC4         QARLQHL---------SSLESS---------FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1         QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3         RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5         RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A        LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA        LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat         ------------------KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4         LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1         LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3         LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5         LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA

HC2A        KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA        KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat         KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4         KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1         KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3         KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5         KFGDLLFEEEVEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

HC2A        LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA        LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat         LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4         LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1         LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3         MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5         MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY
```

A

FIG. 3
3 of 5

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                                                                       Transmembrane
HC2A   ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA   ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat    ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4    ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1    ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3    DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5    DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKCYTEAAMCLVHA

        domain                       SH3
HC2A   TALVAEYITRKGV-----------------------------------FRQGCTAFRVITPN
KIAA   TALVAEYITRKEA----------VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat    TALVAEYITRKEAD--------LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4    AALVAEFIHRKKL-----------------------------------FPNGCSAFKKITPN
HC1    AALIAEYIKRKGYWKVEKICTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3    AALVAEYISMLED-------------------------------------RKYLPVGCVTFQNISSN
HC5    AALVAEYISMLED-------------------------------------HSYLPVGSVSFQNISSN

                                                             ITAM
HC2A   IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
KIAA   IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
rat    IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4    IDEEGAMKEDAGMMD-------VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1    IKEEGAAKEDSGMHD-------TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3    VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5    VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI

                 ITAM     ITAM               ITAM            ITAM
HC2A   YEKRRD--------------------------------------------------------
KIAA   YEKRRDFERLAHLYDTIHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat    SMKSGGTLETTHLYDTIHRPYSKVTEVITR-----------A----AGSWDLLPGGLFGQ
HC4    YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLLG-------------TFFRVAFYGQ
HC1    FEKQRDFKKLSDLYDIHRSYLKVAEVVNSEKRLFG--------------RYYRVAFYGQ
HC3    HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG--------------TYFRVGFYG-
HC5    LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG--------------TYFRVGFFG-

                ITAM                 ITAM
HC2A   -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA   GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat    GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4    SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1    GFFEEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3    TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5    SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQGFGAEFVEVIKDSTPVDKTKLDPNKA

       ITAM
HC2A   YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA   YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat    YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4    HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1    YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3    YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5    YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT
```

A

FIG. 3
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                                                    Coiled-Coil 1
HC2A        IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA        IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat         IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4         SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSTDVDMIQLQLKLQGWV
HC1         SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3         SHAFPYIKTRVNVTHKEEIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQGSV
HC5         MHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSV

                                                                Coiled-Coil 2
HC2A        SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLF
KIAA        SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLF
rat         SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLF
HC4         SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSLALELNERLIKEDQVF
HC1         SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLF
HC3         GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKF
HC5         GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRF

  Coiled-Coil 2
HC2A        YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
KIAA        YQEEMKANYREMAKELSEIMHEQLG----------------------------------
rat         YQEEMKANYREIRKELSDIIVERICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILS
HC4         YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAISGTSSDRGYGSPRYA
HC1         YQEELRSHYKDMLSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKATPALPTVSISS
HC3         YQRELG----KLSS----------PZ----------------------------------
HC5         YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

            PBM
HC2A        SSVVZ-------------------------------------------------------
KIAA        -------------------------------------------------------------
rat         CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4         EVZ---------------------------------------------------------
HC1         SAEVZ-------------------------------------------------------
HC3         -------------------------------------------------------------
HC5         -------------------------------------------------------------

HC2A        -----
KIAA        -----
rat         VHIFF
HC4         -----
HC1         -----
HC3         -----
HC5         -----
```

A

FIG. 3
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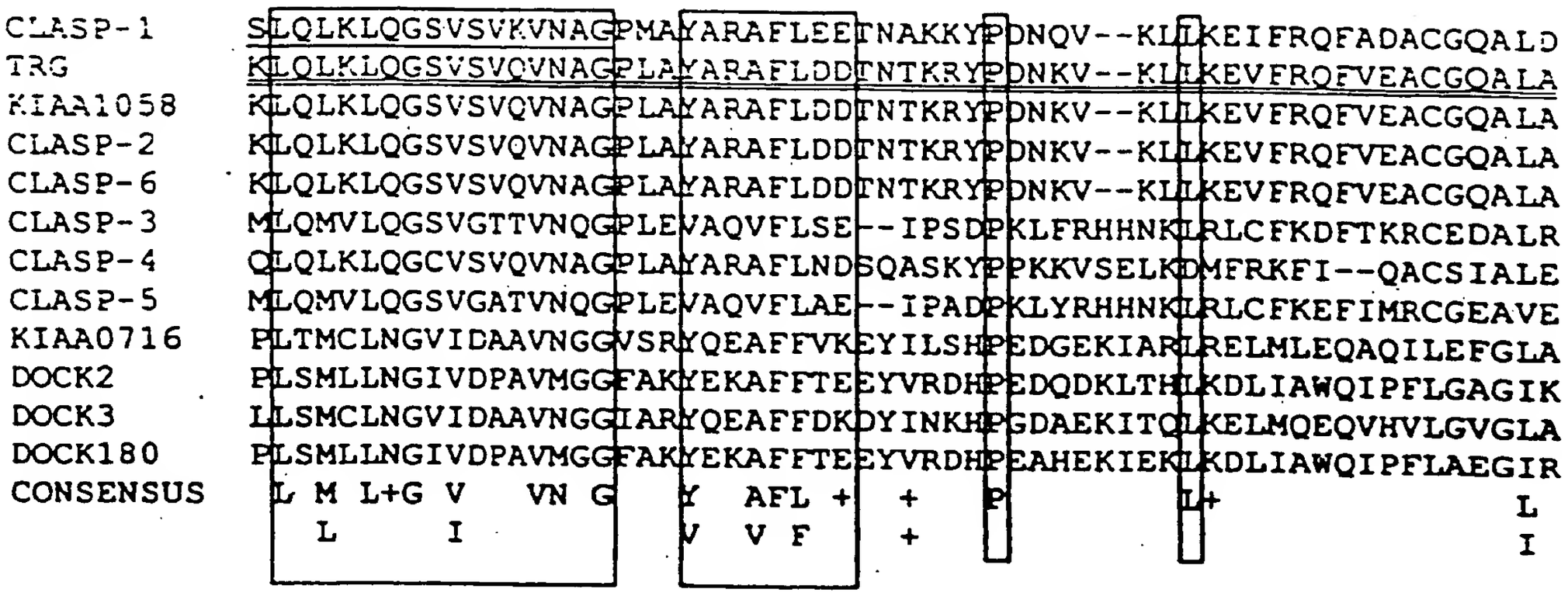
```
                A                                   B
CLASP-1     YRVAFYGQ::::::::::::::GFFEEEEGKEYIYKEP
KIAA1058    FRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEP
CLASP-2                               FEDEDGKEYIYKEP
CLASP-6     FRVAFFGQ::::::::::::::GFFEDEDGKEYIYKEP
CLASP-4     FRVAFYGQ::::::::::::::SFFEEEDGKEYIYKEP
DOCK180     FAVGYYGQ:::::::GFPTFLRGKVFIYRGKEYERRED
DOCK2       FAVGYYGQ:::::::GFPSFLRNKVFIYRGKEYERRED
DOCK3       FRVGFYGR::::::::::::::KFPFFLRNKEYVCRGH
KIAA0716    FRVGFYGK::::::::::::::KFPFFLRNKEFVCRGH
CLASP-3     FRVGFYGT::::::::::::::KFGDLDEQEFVYKEP
CONSENSUS   F V FYG                     KEY  K
                YF                      Q F  R
```

```
                                                                   C
TRG         PKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAYIQVTHVTPFFDEKE
CLASP-1     PKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYAYIQVTYVTPFFEEKE
CLASP-2     PKLTPLSEISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKE
CLASP-4     PKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYAHIQVTYVKPYFDDKE
CLASP-3     PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDTYE
KIAA0716    HDYERLEAFQQRMLNEFPHAIA------MQHANQPDETIFQAEAQYLQIYAVTPIPESQE
DOCK3       HDYERLEAFQQRMLSEFPQAVA------MQHPNHPDDAILQCDAQYLQIYAVTPIPDYVD
DOCK2              FQMQLMTQFPNAEK------MNTTSAPGDDVKNAPGQYIQCFTVQPVLDEHP
DOCK180     EYERREDFQMQLMTQFPNAEK-------MNTTSAPGDDVKNAPGQYIQCFTVQPVLDEHP
CONSENSUS       L     L  Y                                 YIQ+   V P  D
                      M  F                                  L          E
```

```
              D                       E
CLASP-1     RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN
TRG         RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH
KIAA1058    RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
CLASP-2     RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR
CLASP-6     RTILTAIHCFPYVKKRIPFMYQHHTDLNPIEV:HDEMSKKVAELR
CLASP-4     RTILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELQ
CLASP-3     KTILTTSHAFPYIKTRVNVTHKEEIILTPIEVAIEDMQKKTQELA
CLASP-5     NTVLTTMHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLA
KIAA0716    RTSLYLVQSLPGISRWFEVEKREVVEMSPLENAIEVLENKNQQLK
DOCK2       RTSFVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL
DOCK3       RTTLTLTHSLPGISRWFEVERRELVEVSPLENAIQVVENKNQELR
DOCK180     RTSFVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL
CONSENSUS   RT L     FP V   + V        + P+E AI+ M     +L
               F     L  L                        +      I
```

B

FIG. 3
1 of 2



DOCK1=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1056

B

FIG. 3
2 of 2

1
A

```
2                                                  32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG

62                                                 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC

122                                                152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA

182                                                212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
                    met asp arg ser cys asn arg met ser ser his thr glu thr ser

242                                                272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302                                                332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp
          ref 1.1 and 1.2
362       ref 2.1 and 2.2                          392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

421                                                452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482                                                512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542                                                572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602                                                632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
                    ref 3.1 and 3.2
662                                                692
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722                                                752
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro
                          ref 4.1 and 4.2
782                                                812
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys
```

A

FIG. 4
1 of 15

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842                                                 872
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

902                                                 932
GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT
val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his

962                                                 992
AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022                                                1052
TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082                                                1112
ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142                                                1172
ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val

1202                                                1232
GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu
                  ref5.1 and 5.2
1262                                                1292
ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322                                                1352
ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

1382                                                1412
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1442                                                1472
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1502                                                1532
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu
                                    ref 6.1 and 6.2
1562                                                1592
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1622                                                1652
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu
```

A

1682 1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1742 1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1802 1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

ref 7.1 and 7.2

1862 1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1922 1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1982 2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2042 2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2102 2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

2462 2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

A

FIG. 4
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ref 8.1 and 8.2

2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2702 2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

ref 9.1

2762 2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

ref 10.1 and 10.2

2945 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

ref 11.1

3242 3272
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

A

FIG. 4
4 of 15

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3302                                                    3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

3362                                                    3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422                                                    3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482                                                    3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

3542                                                    3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602                                                    3632
TGG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro OCH

3662                                                    3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722                                                    3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782                                                    3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842                                                    3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902                                                    3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962                                                    3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022                                                    4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG
                                                        ref 12.1
4082                                                    4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142
CTC
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A

FIG. 4
5 of 15

Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 364-380.

TTTTTTGAATTAATGGTGAGCAAAAAACTGAGCATGTTCTTTAATATTTTTTTCTCTTAGTG
AACAATTTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAAACTTGTGATACATTCTTTG
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGG
AAAGAGCTTTATAGATACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG
CCAGTTACAATCAATAAAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATCACTTGAGATCAGGAGTTTGAGAC
CCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAAAATTTTTTTTTTAAAT
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG
TTNTGATTCNACACNTGCAACTCCCGCATTGGGTNAACAAAANCCAAGGAANC.

Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 371-380.

AATTAATGGTGAGCAAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTGAACAAT
TTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTCTCAGG
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAAACTTGTGATACATTCTTTGCTAGT
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGGAAAGA
GCTTTATAGATACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT
NCAATCAATAAAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC
AGCACTTTATAAGGCCCNAGGCNGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG
CCTGGGCAACATANCAAGAGCCCATTATCTACCAAAAAANTTTTTTTTTTAAAATTAAG
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCCNATNTNCCTTTGGAAAAGCTTANG
AAGGGGAGGGCTTNCTTTGGANCCCCAAAAAGTTNAAAGGGNTTGCAGTCAGCCTTTT
NAATCACCCNNNGGNCCTNTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT
CNTNTTTTAAAAAANTNTTTTAAAGNANNTTTNTTNGN

A

Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is underlined and represents nucleotides 381-385.

TCTTTNNGAAAAAGATTANATTATTAATTCTATGATATATTAACAATACACANCTCTAA
CACTTGGACTATTTTTAAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC
TTCTCAAATATTTTTTAAAGTTCCCTACAATGTTTTGTATTTGCTTAAAATAAAATANA
AAAACCACCATATTACTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT
GTGTATGTCAACAAAAAAAAATTCAACCTTAAATTTTTTTTTTTTCCATAAAAAACAGGGC
TACTTGCCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA
NTGTCGGNCCCTNCGTTTAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCNNACTNTTNN
NCNCCCATCTTTNCNNTTNNNNNCCCCCNTTTNNATNNTTTNNNTNNCNNNNNNATNT
NTNAANNNACCNCC

Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequnce matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA
AAACCCCATATTACTTTCAGAAAANTATGCTAGCTAACAATAGGACANAAAAATTCTG
TGTATGCAACAAAAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAACAGG
GCTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGCT
AAGCGTTCTTGCCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAAA
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC
CGAATGGNATCTATTCCGGGAGACANATTACTATNGGATGANAGCANATNGCCCNNAT
GCTTNTTTGTAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNNT
NNGCGANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNTGANTGNCT
GGGAGAACCTACNTNCCCCNTACNNATANNCTNCACCCCCTACTACTNTNNCNNTCNC
TCTCTANTTCTACTCCACNTTATTATCCTCNNCCTTCNCATCNTCCCATCNTNATTCNAC
GCCNCNANACTTANCNTTNATNCACTCTNNCT

A

Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-733.

<u>TAATGTACATAGTGCTCATGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACA</u>
<u>C</u>CAGAACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCA
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAAACTATCAGGTTTACT
GTATAAACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAA
TATTTCTACTTCTCATAAAACAGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC
TTCCTTCTTAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCTGTATTTAT
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAGGTTT
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGG
GTGAGGTGCCCCATGCCTT

Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-730.

<u>TAACATAGTGCTCTGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACA</u>CCAGA
ACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC
ACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAAACTATCAGGTTTACTGTATA
AACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAATATTT
CTACTTCTCATAAAACAGGGAAAACGTATNTCACCAAAAATAACTTCTTATTACTTCCT
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGAGACATACTATTAAACCT
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA
TAAAGGTTTTNGGGGGAAAAGGGAAAAAAATNGATTNCATNTCGNGGTTNGCAAGGTN
TTTTCCATTGNGGGGNGGAGGGGCCCATGCCATAANTTTTAACCTTTCTTTTTTTNGAAG
AAATTAAACNNTTAAAGGGGTN

Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-917.

A

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGCACAAGCTCTCAGCA
GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA
CTTTAGCTTTGGGCAGGAACTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA
AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCCTTATCTTAGCCTTTATCCCCTTGT
GGAAAAGACACTATCAATGCTAGATNCTCCCAAGNCAGAGAATTATGCAGGTTTGGTC
AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT
TTTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNGGGTCTAGGACAT
AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTTNG
ANANGAATNNNCTGNGAAGGGCCCGATACGANAATTTGACTTCGGNGAAAATTNNNG
GATTNNTACAAANTTCTAGGNGGCACCTTNAAAANGNNTGGGNACNTTGGNGGCGGA
AAAAAAGCCCTTCNTTTAGNTNTCCCNGAAATGGAAAAGTNCCAANTTCCNAAAAAA
ANGGGCTTTGTTNNCTTNCNANA

Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-921.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGGAAGGCCGATATCAACTATT
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT
ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA
TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACTTGTGGATGNTTATAA
GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTCTTTTCC
TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG
NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT
GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC
TATNGANTATGNGGTTCTAGGACATGATTACATTTTTNGGGAACTTCCATAGAATAAA
CNTNTACCTNAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAGTNC
CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGGNCTTTAGNACGT
TNGATNTTTGANCGGAAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC
NAANAAGGNCTGTGTTNTTNGACATTTACCNGNNCCNTTTCTAATCAAACNTNCTCTTC
TNNNANCCNCANCNCNNNCCTATANNCCTATCNCTCNNCTNNNCTCNTCACTCTCNNC
NCTNTCTTCCNTTCTNCACTNTNNNNTCNCTNNNATNNNCTTCTCCNATCCNTCTCANN
NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCCT

Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1181-1269.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAAC
AAGGCCTGGCAGTTTCCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTTT

A

TTTTCTNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTAT
CAGCTGATGCAAAAGTGCTCAGTTTTATTTATGAAAATATTAAAGTTCCCAGAATATTA
ACTGTCTTCTCCCAAACAGTTTTAAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGC
CCCGTATTCTGCATTCAGAATTTGGAAAATTGCCTCATTATAGATAGCCATNTCTTTTTT
TTNTTTTTTTTTATNCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACA
TATGTATACATGTGCCATGTTGGTGTGCTGCACCCANNAACCCGCAATTTAACATTAGG
TNTATCTCCAAATGCTATCCNTTCACCCTTCCCCCATNCCACAACAAGGCCCCGGGCNT
TGNGATGTTCCCCTTCCTGTGCCCACTGTGTNTCACATTNCCNCTTCCCNCCCTTANTN
NNGTGCAGAACNTNGCCNGTNGCCCTNTNTTTTTNNCCC

Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1151-1269.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGC
AATCGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCA
ACGGTAAAAACAATCCTCCTACAGAATTTTTTTTTCTAGAAAGACAAATATTTACTAGG
ATATGCCCTTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTT
ATTTATGAAAATATTAAAGTTCCAGAATATTTAACTGTCTTCTCCCAACAGTTTTAAAA
AATGATACCTCAGGTTTATGGGGAAAAAAGCCCCGTATTCTGTCATTCAGAAATTTGG
AAAATTTGNCTCATTATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTTTTATACNTTTAA
AGTTTTTAAGGGGNACCATGTTGCACCAAAANATTGCAGGGGTTNGGTTACCATTATGG
TTATTNCCATTGGTNCCCCCANTGTTTGGGGNGTTGGCTTTGCCACCCCCCAGNGTAAA
ACCNNCCGNTGCGAATTTTTAAAACAANTTTTGGGGGTTATTANTTNTTTCCCAAAAAT
NGGCNTTTTTNCCCTTTNCCCCCCTTTCNCCCNCCCNNTTCCCAACNNANCAAGGGGCC
CCCCGGGTANTGGGGGAATAGNTTTCCCCCCCTTNCCCTNGNNGGGCCAATTGTGGGG
NNNCTCCATTTGGNNTGCAAANTTCCCCCACCCNTNATTGTTGGTGGNGAAACCATTTC
CCGGGGGGTTTGGGGGTTTTTTTTTGGTCCCCNTTGCCCAANTAATTTTTGCNTTGAANA
AAAAGAATGGGGTTTTCCAAAGCTTTTNGTCNCCATTTGNTCCCTTTANGGNNCCNTTN
GTTCNCCTTNCCANAANGGGCCAATGTGAAACNNCCTTTCATTTTTTTTTTATTGGGGNT
TNCCNTTATGGN

R f 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1535-1588.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCG
GTACGTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTTCCTTGAGTTGTAT
ATTGTAATGATCATTGTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTT
TAAGTGTAACTGTGAATTAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAAT

A

TCTGATTTAGGTGAGTCAGCATACCGCCCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTC
TAGAAAACGTTCTCTAGAAAGTCCTATCTAGAAAACTTTCTCTAGAAAGTCCTTATGTG
ATTAATAGCATCCATCCTCCCTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGT
TCACAGCAAAAGTGAGCAAAGGTACAGAGATTTCCCATATACCCCTTAGTATGCGTAG
CCTCCCCCATTATTAACATCCCCCATCAAGAGTAGTGCATTTGTTGTAACTGGTGAACC
TACATTAACACATCATCACCCAGAGTCCGCAGTTTACATTAGGGATCATTCATATAACA
TCTATTTTTACTTTTTTTTTTTTTAGTTGAGACAAGATTCTCGCTCTGTCACCCAAGCTGG
AGTGCAGTCCGNGTGGATTGTNGGCTTACTGNCN

Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1547-1588.

<u>GTGCCGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGG</u>GTACGTACACAATAGC
TTCTCCTCCTGGTGAGAATTTCTTCAATTTCCTTGAGTTGTATATTGTAATGATCATTGT
TGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTTTAAGTGTAACTGNGAA
TTAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTAGGTGAGT
CAGCATACCGCCCCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTA
GAAAGTCCTCTCTAGAAAACTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATC
CTCCCTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTG
AGCAAAGGGCAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTAA
CATCCCCATCAGAGTAAGNGCATTTGTTGTAACTGGNGAACCTACAATTNACACATTN
TNACCCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCTANTAACACCTATTT
TTTTACTTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAA
ACTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTG
CNNTCNNCTTNNCNCCNAAAGAANTTTTTTTTCACCCTTTTTTTTTCCCCCNAANANANN
ANCCTTCCCCTTGGNGGANGCTGGGGACTTCCNCAGNGGNGG

Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1861-1917.

<u>CAAAGTGCAGTTTATCTCAACACTGTTTTGCTCACAGAGAGCCTTGGTTTCAAAGG</u>GTAG
GTTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATC
ATTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA
AATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCCTT
TTAGAATTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAAC
TTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG
TTTTCTCTTCACTTGGTTCTGTTTTTATAAAAAACTCAATTTATAAAGAATTCAATATAT
AAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTTG
TTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATTCTT

A

AAATTTTGAAGGTAGCTATTCATTTTAATCATCCTAGAGGATGGAATGCANAGATGTT
GGATGAAAAATAACTTACGTATTATTTTGTAATAAATATAAGAATTCATATATGGTTGAT
TACCTAAGTGGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNTNGA
TATATTATTT

Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1864-1917.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTCAAAGGTAGG
TTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATCA
TTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAAA
ATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCCTTT
TAGAATTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAACT
TGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTGN
TTTCTCTTCACTTGGTTCTGTTTTTATAAAAAACTCAATTTATAAAGAATTCAATATATA
AGCCATTCACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTGTT
CACCTGCTTTAAAATGNGACNTCNTAATATTTTGGNTTTCCCCTTAAGAAAATATGTAT
AATCCTTAAAANTTTNGAAAGGGANGCTANTTTCATTTTTTNAATCAATCCTAANAGG
GATTGGGAAATGCNCAAGATTTTTTGATTGAAAAANAACCTTANCGNATTTAATTTTTN
GGNAATAAAATAATTAGNAATTCCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTAT
TGCCCCCATTTCNTTGATATGNAAAGCCTTTCACCAACCAAATTCCCCNTTGNNAGGAAT
ATTATTTTTTNANGGGCCTCNTNTTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAAAG
GGTCCCCNC

Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2432-2523.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAA
ATATCTTCCTGTGGGATGTGTAACATTTCAGGTAGGAATCTTCCAGATGTACATTAAAT
CAAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTAGTTTAT
AAGGAAAGCTTAAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTCACAGTG
ATTGTCATTAATACATTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTA
CCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCTTGNAATCCC
GTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATT
CTTAATTGGCTTTTACTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATAAA
ATATTAAGATTATTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAGTA
GGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCTTG
CTTTTTCTTCAAAACCTGTTAAATAGTAGGNTTGGGGATATTNTAAAAATTAGGTAAAT
GGTATATCTTCTGGTGGAAANCAGAAN

A

Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2444-2523.

<u>CAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGT</u>
<u>GGGATGTGTAACATTTCAG</u>GTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATC
TTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTTAGTTTATAAGGAAAGCTT
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTCACAGTGATTGTCATTAA
TACATTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTACCTCTGAATTA
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTTT
AACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCTTAATTGGCTT
NTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAATATTAGGATT
ATTTTATGACTAATACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAAT
TTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAAGTCANTTATGCCTTTGCTTTTTCT
TCAAAACCCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAATTTCAAGCT
NAAANTGGNTTATTATTCNTTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNAA
NAAAAAAGNTTATTCCNGGTTTCTTTNCGGNAAAAAAACCAAAAAATCTTNGAAATTGT
TTTTTACCAAAAANGACCTCCNCNGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACN
N

Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2679-2698 of the cDNA. Exon sequence is underlined and represents nucleotides 2711-2799.

<u>TTCCTATTCATGAAGCTAATCGGGATGCAAAGAAACTATCCACAATTCATGGTAAACT</u>
<u>TCAAGAAGCATTCAGCAAAATTGTTCATCAG</u>GTAATGATTCCAATTTCTAGCTTCACTA
TAAAGGGAAAAAACTGTCTGAAAGCATTAATGTTGTTTTGCACTGATGTCAAACTAGA
TCCCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAAATGATAGTTCAT
GGCCAAAGCAAAGCTCATTAACAATAAAAATGAATTCACCTAAAGTAAATGGTGATCA
TCATAAACTTTCTGCATAGCTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTT
TAAAAATTGTGATTTTCTGTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTT
AAAAAATTGATACCCTATTNCTTTTGCTGNGGAAAANTGGAAGTTTTTTAATATTTTCAA
GGTTTTTTTTTAAAATTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAAACCTAC
CTAAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACCNTTTTATTTTTTTCCCCTAG
GAATGGTTTTACCCAAATCCATTCCCTTTTGAATAATATTTTTCCCTNAATTNCCCAAA
AAANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGGAAAATTAAAAAAAATGGGGGTGG
GGCCNTAAATGGGGATTATTTTTAAATTTCCTAAAAAAGGGANTTTTCCATTTACCTTT
NAATCCTTTTTGGGNGGNTTCNATTTATTGGGGAATCCTNCNCTTTTTTTNTNCNCCTTA
AAAAANTTAGGGCCTNCCAAAATTTTAAACCNTTTAATTTTTTNAAAANGGAAAGGGNC
CCCTTTCTTNGCCCGGTTGGTTT

A

FIG. 4
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Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2928-2941.

<u>TACAGATTGGAGG</u>TGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT
CTCTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT
CTTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGAGACTATTTTCACACAT
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA
TAATCCCACATTTTGTTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTA
GAACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTT
CCAGGTGAGGTTTCTTTAGAACGTAAAAGCCTGAAATCACACCTTAAAAACACTTCCT
TTAACCTTTATAATTTCTTAATTTTCACCATAAATGATTGCGTTTTATATTTACTGGGGC
TAACTAGNATTTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTGTTACTCAA
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTCACCTGGGAGAATGGTTGGNAATGC
CAGAACCCTTAGACCCCACCCCAGCCCCTGTGAAA

Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2930-2941.

<u>CAGATAGTAGG</u>TGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT
CTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT
AAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAATCT
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGAGACTATTTTCACACATAT
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA
ATCCCACATTTTGTTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTTGAACTAG
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTTC
CAGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTT
TAACCCTTTATAANTTNCTTAATTTTCACCCATAAAATNGATTGCNGTTTTATATTTTAC
CTNGGGNCTANACCTNAGGCAATTTTTCTGGGTCATAAGGGAAATTTCTTTTTCCCAAA
CCCTTTTCTTCTTATTTTGTTGGGNCACCTCCCAAAAGGTGNTCNGTTGGGGNTTNGGG
NCCCCGNGAAAGGCCATTTGGGGGNTTCACCCCCGGGGGANGATTTGGTTTTGGAAAA
TNGTCNNNAAAACCTTCCNNACCCCCNNCCCCCNGGCCCCCNTGNNNGGAAATCCAAA
AGGATCTTGNCNATTTTTTTANCCAAANGANCNCCCCCNAGGGNGGGATTTTNGTTAT
TTCCCCAANAAGANGTAAGGTTNTTGGCCTTTNGGGGCNTTGGGTGTTTTTNTTTNN

Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3376-3393 of the cDNA. Exon sequence is underlined and represents nucleotides 3267-3289.

A

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA
TCGGTGTTAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAA
CTATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAAAAGATCAATNGT
AAACTTCATGTAACAATAAAATTCCAAACTTGGATTCTAAATGAANNAAAAANATCAA
CCTTTAAAGAAAAGCTGGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGA
CTCAAAATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCT
GAGTGGTGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTT
TAGGCATGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCC
TGCCGCTNAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNG
NAAGNGNTCCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTC
AGNGCTTCTTGCACCTCCTGNGCATCTCCCGTANTTCACCCTCATTNNACCNTNANTTT
ATAANNANNNAGCCCACNTNNCCTATAGGCNATCNACGCNNTTCCCNNTANTCANTNN
NAGACAATTTTTTNNCGCCCCCTCCTNNTCCTTCCTNNCTTCCNCCCNNCNNCCCTNTN
TCTNTNCCCCCNCCNNTTCTTANCTTNCT

Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3750-3769 of the cDNA. Exon sequence is underlined and represents nucleotides 3779-4118, and also represent the 3' terminus of the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATT
GAAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATG
GCTATGGTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTTAAGACATTTTAATGACTC
AAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTATTCA
CTTTAAGTTCGTATTTTTTAATTTATATTACCATTTATAGATTCATTTTGGAACCATTTT
AAATGTAGTAATGCTTATTTTAAAGGTACTATTAAATATGTGAATGTTTACACTAATTT
TACCGAGTGGGACTTCAAAATTTTTATTATTGACAATGGCTGAGAACAATTNAAGGGT
TTGACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATT
AATGAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTTACATACCCAAAAACAGGAA
ATTTTAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATN
TANTNTTAAAATTCCCGGGGGGGANTAATCTTAATNACCCCGGGTGGGGCCANNCNCCC
CNTTATAACTTTGGAATTTAAAAATTCNTTTTTTTNTNCAACCCCAAACTGNANTNGGGT
NNTTTTNAAGGAAAACCTTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCCTNCNAN
AAANNGGGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCAAAAAATTCT
TAATAAAANCCCCGGGGCTCCCATTNTTAGNATTTTTTTTTTTTGGCCCCACACTGTGTT
NATTAAANCCCCNCNTGCTAAAAATTTTTNNNGAAAANACCTNAACCCTTCTNNA

A

```
HC2A    ----------------------------------------------------------
KIAA    ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat     ----------------------------------------------------------
HC4     ----------------------------------------------------------
HC1     ----------------------------------------------------------
HC3     ----------------------------------------------------------
HC5     ----------------------------------------------------------

HC2A    ----------------------------------------------------------
KIAA    FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat     ----------------------------------------------------------
HC4     ----------------------------------------------------------
HC1     ----------------------------------------------------------
HC3     ----------------------------------------------------------
HC5     ----------------------------------------------------------

HC2A    ----------------------------------------VLHHHQNPEFYDEIK
KIAA    KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat     ----------------------------------------------------------
HC4     ----------------------------------------------------------
HC1     ----------------------------------------------------------
HC3     ----------------------------------------------------------
HC5     ----------------------------------------------------------

HC2A    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat     ----------------------------------------------------------
HC4     ----------------------------------------------------------
HC1     ----------------------------------------------------------
HC3     ----------------------------------------------------------
HC5     ----------------------------------------------------------

HC2A    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat     ----------------------------------------------------------
HC4     ----------------------------------------------------------
HC1     ----------------------------------------------------------
HC3     ----------------------------------------GPGPARSTVSISLISNSARV
HC5     ----------------------------------------------------------

HC2A    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat     ----------------------------------------------------------
HC4     ----------------------MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1     ----------------------------MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3     NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5     ----------------------------------------------------------
```

B

FIG. 4
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```
HC2A   IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTK[illegible]TILKPSADFLTSN
KIAA   IIHVVAQC[illegible]LESHLRSYVKYAYKAEPYVASEYKTVHEEL[illegible]TILKPSADFLTSN
rat    ------------------------------------------------------------
HC4    LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1    LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3    TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5    ------------------------------------------------------------

                                    Cadherin
                                    Cleavage
HC2A   KLLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA   KLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat    ------------------------------------------------------------
HC4    KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1    HVLKHSWFFFAIILKSMAQHLIDTNKIQLPRPQRFPESYQNELDNLVMVLSDHVIWKYKD
HC3    SALQQAWFFFELMVKSMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK  1.1/1.2/2.1/2.2
HC5    ------------------------------------------------------------

HC2A   NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA   NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat    ------------------------------------------------------------
HC4    IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1    ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLCQYKFDFL
HC3    DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVIVSLRLDFL  3.1/3.2
HC5    ------------------------------------------------------------

HC2A   RVVCNHEHYIPLNLPM-----PFGKGRIQR------------YQDLQL----DYSLTDEF
KIAA   RVVCNHEHYIPLNLPM-----PFGKGRIQR------------YQDLQL----DYSLTDEF
rat    ------------------------------------------------------------
HC4    QTICNHEHYIPLNLPM-----AFAKPKLQR------------VQDSNL----EYSLEIEY
HC1    QEVCQHEHFIPLCLPIRSANIPDPLTPSES------------TQELHASDMPEYSVTNEF
HC3    RIICSHEHYVTLNLPCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF  4.1/4.2
HC5    ---------------MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

             Cadherin
             EC motif
HC2A   CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA   CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat    ------------------------------------------------------------
HC4    CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1    CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3    RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAM
HC5    SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA

HC2A   LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA   LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat    ------------------------------------------------------------
HC4    LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGELS
HC1    LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
HC3    LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE-----------SG---SMIS
HC5    LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----------GA---GAIT
```

B

FIG. 4
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```
HC2A    KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDHQQSS
KIAA    KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKQQSS
rat     ------------------------------------------------------------
HC4     TDKDTAYGSIAG--------HGIKREDSRGSLIP-EGATGFPDSTGEN-----TRQS
HC1     KDVLNSIAAFSS------IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3     QTVAMAIAGTSVPQ--------------------LTRPGSFLLTSTSGRQHT---------
HC5     QNVALAIAGNNFN---------------------LKTSG-IVLSSLPYKQYN---------

HC2A    TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA    TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat     ------------------------------------------------------------
HC4     STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1     ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIEVCL
HC3     ----------TFSAESSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLYLCV
HC5     ----------MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A    HQFQYMGKRYIARNQEGLG--PIVHDRKS----------------QTLPVSRNRTGMM
KIAA    HQFQYMGKRYIAR---------------------------------------TGMM
rat     ------------------------------------------------------------
HC4     FHFRYMGKRNIARVHDAWLSKHFGIDRKS----------------QTMPALRNRSGVM
HC1     QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3     SCFEYKGKKVFERMNSLTFK--KSKDMRAK--------------LEEAILGSIGARQEMV
HC5     LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR--------------LEEALLRGEGARGEMM

HC2A    HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA    HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
rat     ------------------------------------------------------------
HC4     QARLQHL---------SSLESS---------FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1     QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3     RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5     RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A    LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA    LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat     ------------------KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4     LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1     LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3     LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5     LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA

HC2A    KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA    KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat     KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4     KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1     KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3     KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5     KFGDLLFEEEVEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

HC2A    LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA    LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat     LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4     LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1     LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3     MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5     MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY
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B

FIG. 4
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Refs

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                                                    Transmembrane
HC2A  ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA  ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat   ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4   ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1   ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3   DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5   DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHA

      domain                     SH3
HC2A  TALVAEYILTRKGV--------------------------------FRQGCTAFRVITPN
KIAA  TALVAEYILTRKEA---------VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat   TALVAEYILTRKEAD------LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4   AALVAEFILHRKKL--------------------------------FPNGCSAFKKITPN
HC1   AALIAEYIKRKGYWKVEKIGTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3   AALVAEYISMLED------------------------------RKYLPVGCVTFQNISSN   8.1/8.2
HC5   AALVAEYISMLED------------------------------HSYLPVGSVSFQNISSN

                                                      ITAM
HC2A  IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
KIAA  IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
rat   IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4   IDEEGAMKEDAGMMD-------VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1   IKEEGAAKEDSGMHD-------TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3   VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5   VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI

                   ITAM   ITAM                 ITAM         ITAM
HC2A  YEKRRD------------------------------------------------------
KIAA  YEKRRDFERLAHLYDTIHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat   SMKSGGTLETTHLYDTIHRPYSKVTEVITR-----------A----AGSWDLLPGGLFGQ
HC4   YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLLG--------------TFFRVAFYGQ
HC1   FEKQRDFKKLSDLYYDIHRSYLKVAEVVNSEKRLFG--------------RYYRVAFYGQ
HC3   HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG--------------TYFRVGFYG-   9.1
HC5   LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG--------------TYFRVGFFG-

                ITAM               ITAM
HC2A  -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA
KIAA  GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat   GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA
HC4   SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1   GFFEEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3   TKFGDLDEQEFVYKEPAITKLAEISHRLEGEYGERFGEDVVEVIKDSNPVDKCKLDPNKA   10.1/10.2
HC5   SKFGDLDEQEFVYKEPAITKLPEISHRLEAEYGQQFGAEFVEVIKDSTPVDKTKLDPNKA

      ITAM
HC2A  YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA  YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat   YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4   HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1   YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3   YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5   YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT
```

B

FIG. 4

```
                                                  Coiled-Coil 1
HC2A        IHCFPYVKKRIPVMYQHHTDLNFIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQQSV
KIAA        IHCFPYVKKRIPVMYQHHTDLNFIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQQSV
rat         IHCFPYVKKRIPVMYQHHTDLNFIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQQSV
HC4         SNSFPYVKKRIPINCEQQINLKFIDGATDEIKDKTAELQKLCSSTDVDMIQLQLKLQQWV
HC1         SHLFPYVKKRIQVISQSSTELNFIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQQSV
HC3         SHAFPYIKTRVNVTHKEEIILTFIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQQSV
HC5         MHAFPYIKTRISVIQKEEFVLTFIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQQSV

                                                                  Coiled-Coil 2
HC2A        SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA        SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat         SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4         SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE
HC1         SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3         GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5         GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

                Coiled-Coil 2
  HC2A      YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
  KIAA      YQEEMKANYREMAKELSEIMHEQLG----------------------------------
  rat       YQEEMKANYREIRKELSDIIVERICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILS
  HC4       YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAISGTSSDRGYGSPRYA
  HC1       YQEELRSHYKDMLSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKATPALPTVSISS
  HC3       YQRELG----KLSS----------PZ----------------------------------
  HC5       YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGEC-

                PBM
  HC2A      SSVVZ-------------------------------------------------------
  KIAA      -------------------------------------------------------------
  rat       CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
  HC4       EVZ---------------------------------------------------------
  HC1       SAEVZ-------------------------------------------------------
  HC3       -------------------------------------------------------------
  HC5       -------------------------------------------------------------

  HC2A      -----
  KIAA      -----
  rat       VHIFF
  HC4       -----
  HC1       -----
  HC3       -----
  HC5       -----
```

B

FIG. 4
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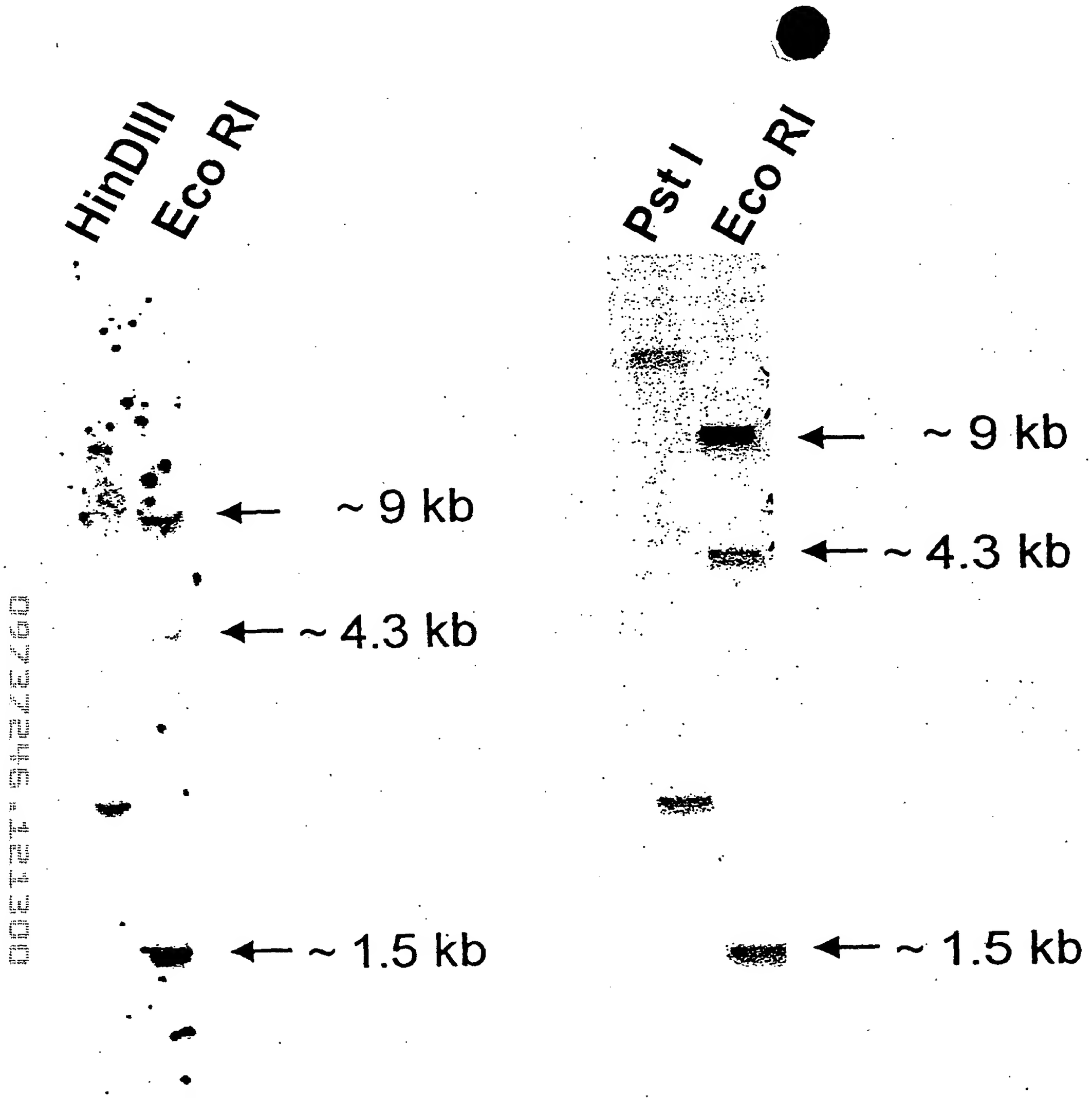
HinDIII
Eco RI
~ 9 kb
~ 4.3 kb
~ 1.5 kb
genomic DNA
Pst I
Eco RI
~ 9 kb
~ 4.3 kb
~ 1.5 kb
BAC 9 DNA

FIG. 5

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-21
GTCGCCGTCGCCGCAGCAGCC -1

1/1                                                 31/11
ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys ile ser arg thr val ala ala glu val arg
61/21                                               91/31
AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT
lys gln ile ser gly gln tyr ser gly ser pro gln leu leu lys asn leu asn ile val
121/41                                              151/51
GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG
gly asn ile ser his his thr thr val pro leu thr glu ala val asp pro val asp leu
181/61                                              211/71
GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT
glu asp tyr leu ile thr his pro leu ala val asp ser gly pro leu arg asp leu ile
241/81                                              271/91
GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu phe pro pro asp asp ile glu val val tyr ser pro arg asp cys arg thr leu val
301/101                                             331/111
TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT
ser ala val pro glu glu ser glu met asp pro his val arg asp cys ile arg ser tyr
361/121                                             391/131
ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC
thr glu asp trp ala ile val ile arg lys tyr his lys leu gly thr gly phe asn pro
421/141                                             451/151
AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
asn thr leu asp lys gln lys glu arg gln lys gly leu pro lys gln val phe glu ser
481/161                                             511/171
GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA
asp glu ala pro asp gly asn ser tyr gln asp asp gln asp asp leu lys arg arg ser
541/181                                             571/191
ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT
met ser ile asp asp thr pro arg gly ser trp ala cys ser ile phe asp leu lys asn
601/201                                             631/211
TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC
ser leu pro asp ala leu leu pro asn leu leu asp arg thr pro asn glu glu ile asp
661/221                                             691/231
CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA
arg gln asn asp asp gln arg lys ser asn arg his lys glu leu phe ala leu his pro
721/241                                             751/251
TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
ser pro asp glu glu glu pro ile glu arg leu ser val pro asp ile pro lys glu his
781/261                                             811/271
TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC
phe gly gln arg leu leu val lys cys leu ser leu lys phe glu ile glu ile glu pro
841/281                                             871/291
ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT
ile phe ala ser leu ala leu tyr asp val lys glu lys lys lys ile ser glu asn phe
901/301                                             931/311
TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT
tyr phe asp leu asn ser glu gln met lys gly leu leu arg pro his val pro pro ala
961/321                                             991/331
GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT
ala ile thr thr leu ala arg ser ala ile phe ser ile thr tyr pro ser gln asp val
```

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FIG. 6
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1021/341 1051/351
TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
phe leu val ile lys leu glu lys val leu gln gln gly asp ile gly glu cys ala glu
1081/361 1111/371
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
pro tyr met ile phe lys glu ala asp ala thr lys asn lys glu lys leu glu lys leu
1141/381 1171/391
AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
lys ser gln ala asp gln phe cys gln arg leu gly lys tyr arg met pro phe ala trp
1201/401 1231/411
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
thr ala ile his leu met asn ile val ser ser ala gly ser leu glu arg asp ser thr
1261/421 1291/431
GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
glu val glu ile ser thr gly glu arg lys gly ser trp ser glu arg arg asn ser ser
1321/441 1351/451
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
ile val gly arg arg ser leu glu arg thr thr ser gly asp asp ala cys asn leu thr
1381/461 1411/471
AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
ser phe arg pro ala thr leu thr val thr asn phe phe lys gln glu gly asp arg leu
1441/481 1471/491
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
ser asp glu asp leu tyr lys phe leu ala asp met arg arg pro ser ser val leu arg
1501/501 1531/511
CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
arg leu arg pro ile thr ala gln leu lys ile asp ile ser pro ala pro glu asn pro
1561/521 1591/531
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
his tyr cys leu thr pro glu leu leu gln val lys leu tyr pro asp ser arg val arg
1621/541 1651/551
CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
pro thr arg glu ile leu glu phe pro ala arg asp val tyr val pro asn thr thr tyr
1681/561 1711/571
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
arg asn leu leu tyr ile tyr pro gln ser leu asn phe ala asn arg gln gly ser ala
1741/581 1771/591
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
arg asn ile thr val lys val gln phe met tyr gly glu asp pro ser asn ala met pro
1801/601 1831/611
GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
val ile phe gly lys ser ser cys ser glu phe ser lys glu ala tyr thr ala val val
1861/621 1891/631
TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
tyr his asn arg ser pro asp phe his glu glu ile lys val lys leu pro ala thr leu
1921/641 1951/651
ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
thr asp his his his leu leu phe thr phe tyr his val ser cys gln gln lys gln asn
1981/661 2011/671
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
thr pro leu glu thr pro val gly tyr thr trp ile pro met leu gln asn gly arg leu
2041/681 2071/691
AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
lys thr gly gln phe cys leu pro val ser leu glu lys pro pro gln ala tyr ser val
2101/701 2131/711
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
leu ser pro glu val pro leu pro gly met lys trp val asp asn his lys gly val phe

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FIG. 6
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2161/721 2191/731
AAT GTT GAA GTT GTT GCT GTT TCG TCT ATC CAT ACA CAA GAT CCT TAT CTT GAC AAA TTT
asn val glu val val ala val ser ser ile his thr gln asp pro tyr leu asp lys phe
2221/741 2251/751
TTT GCT CTG GTC AAT GCT CTG GAT GAA CAC CTG TTC CCA GTC CGA ATT GGG GAC ATG CGA
phe ala leu val asn ala leu asp glu his leu phe pro val arg ile gly asp met arg
2281/761 2311/771
ATC ATG GAA AAT AAC TTA GAA AAT GAA TTG AAG AGC AGT ATT TCA GCA CTG AAT TCA TCC
ile met glu asn asn leu glu asn glu leu lys ser ser ile ser ala leu asn ser ser
2341/781 2371/791
CAG CTG GAA CCA GTG GTC CGA TTT CTT CAT CTT CTG CTA GAT AAA CTG ATA CTT TTA GTT
gln leu glu pro val val arg phe leu his leu leu leu asp lys leu ile leu leu val
2401/801 2431/811
ATT AGA CCT CCT GTC ATT GCT GGC CAA ATA GTT AAC CTA GGT CAA GCA TCT TTT GAA GCC
ile arg pro pro val ile ala gly gln ile val asn leu gly gln ala ser phe glu ala
2461/821 2491/831
ATG GCA TCA ATT ATA AAT CGA CTT CAC AAA AAC TTG GAA GGA AAT CAT GAC CAG CAT GGC
met ala ser ile ile asn arg leu his lys asn leu glu gly asn his asp gln his gly
2521/841 2551/851
AGA AAC AGC CTT CTT GCA TCA TAT ATT CAT TAT GTT TTC CGC CTA CCA AAT ACT TAC CCT
arg asn ser leu leu ala ser tyr ile his tyr val phe arg leu pro asn thr tyr pro
2581/861 2611/871
AAT TCA TCA TCA CCA GGT CCT GGG GGT TTG GGA GGA TCA GTG CAT TAT GCC ACA ATG GCT
asn ser ser ser pro gly pro gly gly leu gly gly ser val his tyr ala thr met ala
2641/881 2671/891
AGA TCT GCG GTG AGA CCT GCA AGC CTT AAT TTA AAT CGT TCT CGA AGC CTT AGT AAT AGC
arg ser ala val arg pro ala ser leu asn leu asn arg ser arg ser leu ser asn ser
2701/901 2731/911
AAT CCA GAT ATA TCT GGG ACT CCC ACG TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG
asn pro asp ile ser gly thr pro thr ser pro asp asp glu val arg ser ile ile gly
2761/921 2791/931
AGT AAG GGT TTA GAT CGC TCC AAT TCC TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA
ser lys gly leu asp arg ser asn ser trp val asn thr gly gly pro lys ala ala pro
2821/941 2851/951
TGG GGA TCC AAC CCC AGT CCA AGT GCA GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT
trp gly ser asn pro ser pro ser ala glu ser thr gln ala met asp arg ser cys asn
2881/961 2911/971
CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA
arg met ser ser his thr glu thr ser ser phe leu gln thr leu thr gly arg leu pro
2941/981 2971/991
ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT
thr lys lys leu phe his glu glu leu ala leu gln trp val val cys ser gly ser val
3001/1001 3031/1011
CGG GAA TCA GCT TTG CAA CAA GCC TGG TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG
arg glu ser ala leu gln gln ala trp phe phe phe glu leu met val lys ser met val
3061/1021 3091/1031
CAC CAT TTA TAC TTT AAT GAT AAA CTT GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT
his his leu tyr phe asn asp lys leu glu ala pro arg lys ser arg phe pro glu arg
3121/1041 3151/1051
TTC ATG GAT GAC ATT GCA GCT CTT GTC AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT
phe met asp asp ile ala ala leu val ser thr ile ala ser asp ile val ser arg phe
3181/1061 3211/1071
CAG AAG GAC ACA GAA ATG GTT GAG AGA CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT
gln lys asp thr glu met val glu arg leu asn thr ser leu ala phe phe leu asn asp
3241/1081 3271/1091
CTG TTG TCT GTT ATG GAC AGA GGA TTT GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG
leu leu ser val met asp arg gly phe val phe ser leu ile lys ser cys tyr lys gln

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FIG. 6
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3301/1101 3331/1111
GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
val ser ser lys leu tyr ser leu pro asn pro ser val leu val ser leu arg leu asp
3361/1121 3391/1131
TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA
phe leu arg ile ile cys ser his glu his tyr val thr leu asn leu pro cys ser leu
3421/1141 3451/1151
CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA
leu thr pro pro ala ser pro ser pro ser val ser ser ala thr ser gln ser ser gly
3481/1161 3511/1171
TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
phe ser thr asn val gln asp gln lys ile ala asn met phe glu leu ser val pro phe
3541/1181 3571/1191
CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
arg gln gln his tyr leu ala gly leu val leu thr glu leu ala val ile leu asp pro
3601/1201 3631/1211
GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
asp ala glu gly leu phe gly leu his lys lys val ile asn met val his asn leu leu
3661/1221 3691/1231
TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
ser ser his asp ser asp pro arg tyr ser asp pro gln ile lys ala arg val ala met
3721/1241 3751/1251
TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
leu tyr leu pro leu ile gly ile ile met glu thr val pro gln leu tyr asp phe thr
3781/1261 3811/1271
GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
glu thr his asn gln arg gly arg pro ile cys ile ala thr asp asp tyr glu ser glu
3841/1281 3871/1291
AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
ser gly ser met ile ser gln thr val ala met ala ile ala gly thr ser val pro gln
3901/1301 3931/1311
CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
leu thr arg pro gly ser phe leu leu thr ser thr ser gly arg gln his thr thr phe
3961/1321 3991/1331
TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT
ser ala glu ser ser arg ser leu leu ile cys leu leu trp val leu lys asn ala asp
4021/1341 4051/1351
GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA
glu thr val leu gln lys trp phe thr asp leu ser val leu gln leu asn arg leu leu
4081/1361 4111/1371
GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
asp leu leu tyr leu cys val ser cys phe glu tyr lys gly lys lys val phe glu arg
4141/1381 4171/1391
ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
met asn ser leu thr phe lys lys ser lys asp met arg ala lys leu glu glu ala ile
4201/1401 4231/1411
CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
leu gly ser ile gly ala arg gln glu met val arg arg ser arg gly gln leu glu arg
4261/1421 4291/1431
AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
ser pro ser gly ser ala phe gly ser gln glu asn leu arg trp arg lys asp met thr
4321/1441 4351/1451
CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA
his trp arg gln asn thr glu lys leu asp lys ser arg ala glu ile glu his glu ala
4381/1461 4411/1471
CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT
leu ile asp gly asn leu ala thr glu ala asn leu ile ile leu asp thr leu glu ile

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FIG. 6
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4441/1481 4471/1491
GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
val val gln thr val ser val thr glu ser lys glu ser ile leu gly gly val leu lys
4501/1501 4531/1511
GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
val leu leu his ser met ala cys asn gln ser ala val tyr leu gln his cys phe ala
4561/1521 4591/1531
ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
thr gln arg ala leu val ser lys phe pro glu leu leu phe glu glu glu thr glu gln
4621/1541 4651/1551
TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
cys ala asp leu cys leu arg leu leu arg his cys ser ser ser ile gly thr ile arg
4681/1561 4711/1571
TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
ser his pro ser ala ser leu tyr leu leu met arg gln asn phe glu ile gly asn asn
4741/1581 4771/1591
TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
phe ala arg val lys met gln val pro met ser leu ser ser leu val gly thr ser gln
4801/1601 4831/1611
AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
asn phe asn glu glu phe leu arg arg ser leu lys thr ile leu thr tyr ala glu glu
4861/1621 4891/1631
GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
asp leu glu leu arg glu thr thr phe pro asp gln val gln asp leu val phe asn leu
4921/1641 4951/1651
CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
his met ile leu ser asp thr val lys met lys glu his gln glu asp pro glu met leu
4981/1661 5011/1671
ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
ile asp leu met tyr arg ile ala lys gly tyr gln thr ser pro glu arg leu thr trp
5041/1681 5071/1691
TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
leu gln asn met ala gly lys his ser glu arg ser asn his ala glu ala ala gln cys
5101/1701 5131/1711
CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
leu val his ser ala ala leu val ala glu tyr leu ser met leu glu asp arg lys tyr
5161/1721 5191/1731
CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
leu pro val gly cys val thr phe gln asn ile ser ser asn val leu glu glu ser ala
5221/1741 5251/1751
GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
val ser asp asp val val ser pro asp glu glu gly ile cys ser gly lys tyr phe thr
5281/1761 5311/1771
GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
glu ser gly leu val gly leu leu glu gln ala ala ala ser phe ser met ala gly met
5341/1781 5371/1791
TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
tyr glu ala val asn glu val tyr lys val leu ile pro ile his glu ala asn arg asp
5401/1801 5431/1811
GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
ala lys lys leu ser thr ile his gly lys leu gln glu ala phe ser lys ile val his
5461/1821 5491/1831
CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
gln ser thr gly trp glu arg met phe gly thr tyr phe arg val gly phe tyr gly thr
5521/1841 5551/1851
AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
lys phe gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu

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FIG. 6
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5581/1861                                                    5611/1871
GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
ala glu ile ser his arg leu glu gly phe tyr gly glu arg phe gly glu asp val val
5641/1881                                                    5671/1891
GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
glu val ile lys asp ser asn pro val asp lys cys lys leu asp pro asn lys ala tyr
5701/1901                                                    5731/1911
ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
ile gln ile thr tyr val glu pro tyr phe asp thr tyr glu met lys asp arg ile thr
5761/1921                                                    5791/1931
TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
tyr phe asp lys asn tyr asn leu arg arg phe met tyr cys thr pro phe thr leu asp
5821/1941                                                    5851/1951
GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
gly arg ala his gly glu leu his glu gln phe lys arg lys thr ile leu thr thr ser
5881/1961                                                    5911/1971
CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
his ala phe pro tyr ile lys thr arg val asn val thr his lys glu glu ile ile leu
5941/1981                                                    5971/1991
ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
thr pro ile glu val ala ile glu asp met gln lys lys thr gln glu leu ala phe ala
6001/2001                                                    6031/2011
ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
thr his gln asp pro ala asp pro lys met leu gln met val leu gln gly ser val gly
6061/2021                                                    6091/2031
ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
thr thr val asn gln gly pro leu glu val ala gln val phe leu ser glu ile pro ser
6121/2041                                                    6151/2051
GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
asp pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe thr lys
6181/2061                                                    6211/2071
AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
arg cys glu asp ala leu arg lys asn lys ser leu ile gly pro val gln lys glu tyr
6241/2081                                                    6271/2091
CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA
gln arg glu leu gly lys leu ser ser pro OCH
```

```
AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC
TTCAGTCGAATGAGCTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTCATCTGCAAAGAGCCATGTATTC
AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTCATTGAAGAATGCAGTG
GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTCGGGTAACAAGCTGTTA
TCTTTTAAGACATTTTAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT
TCACTTTAAGTTCGTATTTTTTAATTTATATCACCATTTATAGATTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA
TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGCGCGCCAGGGCCTC
```

A

FIG. 6
6 of 6

A. Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

B. Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

These differences may be found separately or together in various combinations in the differenct human CLASP-3 isoforms

B

FIG. 6

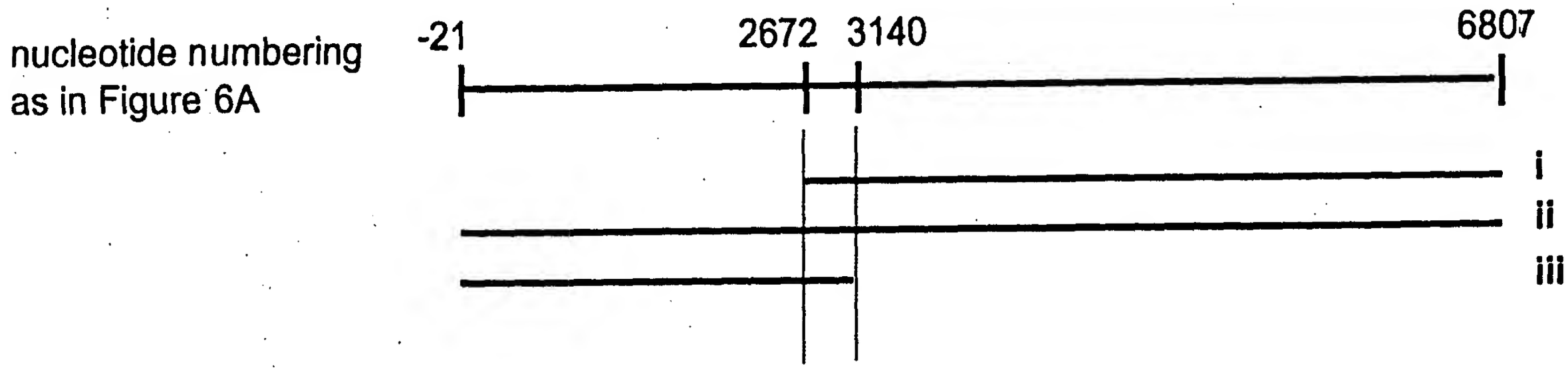
nucleotide numbering
as in Figure 6A
-21
2672
3140
6807
i
ii
iii
469 nt overlap

FIG. 6

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGC
CGCGCCTTCGCCCAGAAGATCAGCAGGTAAATATCCGGCGTGGGGCGC

Exon 85360 - 85510

GTTTTTGCTTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATC
TCCGGACAATATAGTGGTTCTCCCCAACTGCTCAAAAACCTTAATATTGTTGG
CAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 – 94720

TCTTATCCCAACTTTTTACAAAGGTGCCCCTTACCGAAGCAGTAGATCCAGTG
GATTTGGAAGATTACCTCATTACTCATCCTTTGGCTGTGGATTCTGGGCCTTT
ACGGGATTTGATTGAATTTCCTCCAGATGATATTGAAGTTGTTTATAGTCCTC
GGGACTGCAGAACTCTTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACAT
TGACTTATT

Exon 94870 – 94980

TATTTTCCTTTTTAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAG
AAGTTATACAGAAGACTGGGCAATTGTCATCAGAAAGTAAGTTATATGTTTA
TTACAA

Exon 100110 – 100290

ATTTATTTAACTTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTTAA
TCCCAATACATTAGATAAACAGAAAGAAAGGCAAAAAAGGTTTGCCAAAACA
AGTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAA
GTAATACTTTTATTCTTAAATAA

Exon 100340 – 100600

ATATTTAATGTTTTGCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATA
GATGATACCCCAAGGGGTAGCTGGGCCTGTAGTATCTTTGACTTGAAAAATT
CACTTCCTGATGCTTTGCTTCCCAATTTACTTGATCGAACTCCAAATGAAGAA
ATAGACCGTCAGAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACTTT
TTGCTTTGCATCCATCACCAGATGAGGTATAGATGTTTGCATATAAAGAA

A

FIG. 7
1 of 3

Exon 100880-101020

TTTTGGTGTTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTT
CCTGATATACCCAAAGAACATTTTGGTCAAAGACTTCTTGTAAAATGCTTATC
ACTCAAGTGAGTATTTATTTCTTTTACTTACAACT

Exon 112010 – 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTTGCAAGTTTGG
CTTTATATGATGTCAAGGAAAAGAAAAAGGTAAGATTATATAATTTGACCAT
AGTTAT

Exon 113680 – 113880

AAGTTTAACATACTAATATTTTTTAGATTTCAGAAAACTTTTATTTTGACCTTA
ATTCTGAGCAGATGAAAGGGTTGTTACGTCCACATGTACCACCTGCTGCCATT
ACTACCCTGGCAAGATCAGCAATTTTTTCTATCACTTATCCTTCCCAAGATGT
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTTG

Exon 115020-115160

TTAATCTTAACTTTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGA
GACATTGGAGAGTGTGCAGAACCATATATGATTTTCAAAGAAGCAGATGCCA
CCAAGGTAGAATGTTATGCTTCTCATTTCCGCCAC

Exon 117200 – 117410

ATGTATAAAGTTCTGTTTTGCAGAATAAAGAAAAACTGGAGAAACTGAAGAG
TCAAGCAGATCAGTTTTGCCAAAGACTTGGGAAATATCGCATGCCTTTTGCTT
GGACTGCAATCCATTTAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAAG
AGATTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAA
AC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTTGTAGAACGAAAAGGGTCTTGGTCAGA
GAGGAGGAATTCTAGTATTGTTGGCAGACGATCACTTGAAAGGACAACAAGT
GGAGATGATGCTTGTAACTTGACGAGCTTTCGACCAGCTACTCTCACAGTGAC
AAATTTTTTTAAGCAGGTATTGTTCTGTCATGTAGGAATTTT

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FIG. 7
2 of 3

(Next part of CLASP, starting
GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGA
GAAGGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAG)

Exon 5560 – 5710

CTTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATC
TCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACTA
AGACCTATTACAGGTATTTAAAAATTTTGAGTAGAAATGGTTGCA

Exon 6680-6900

TTACATTGTTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTTCTC
CCGCACCTGAAAATCCCCATTATTGCCTAACTCCGGAGCTGCTTCAAGTGAA
GCTTTACCCTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCG
CAAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTTGG
AGAATTCTG

Exon 38920 – 39075

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACC
CTCAGAGTCTTAATTTTGCCAATCGTCAAGGTTCTGCTAGAAATATAACAGTG
AAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA

A

FIG. 7
3 of 3

GTAAGCTGCAGAGTACATGCAAAGTCCTTTCAGACACTTTGGCAACTAGTGAGTCATGT
ATACAAAGAACTATTCAAAGCAAAATGTGGCCAGTTCTCTAAGAGAGTAGTGAAAAGAT
GTTTGGAGAACAGAGATAAAGGCATGCAACATCTGGCTGGGAGTGTGAGAGCAGACAAC
CAATTCAGGGACTATCAAACACCCAGGACAAGCTTAAGTACAGGATGAATAATGACAGT
AACAGTGATAATAATAACAACAGCTGACACACATCGTACTTACCATGAACCAGGCCCTG
TTCTAAGAACTTTATATTAATCAATTCAATAAATCTTCACAACACCCTTTCAAGTAGAT
ATAATTATTTTCCTCCTTTTAGAGATGAAGTTAAGTAGCTTGCCTAAGGTTACAGAGTA
AGAAAGTGGCAAAATAAGTCTGGGTTCCTATCACAGAGGGTCTTAAAAGCCAGGTACAG
TGATAGCCTTGACTTACAGTCTGTGAGTACCTGGTTCATCTTTCCCAATGGACTCAAAC
ATTCTGAGAGCAGGTCTGTGTCTAGTTCACCTTCGTGTTTTTAGAACACCTAGGTGGG
CTCTATACTTAGGTAGAAGCCAAATATCTGTCCTCTTTGAATAGACTATCTTTTCCTTT
AGTAAACAAGCATCTGAAAACAGTGTGTTACTGGAGGGCGCCTTGGCAAGAGCCTGTGG
TACTAGCTACTCCTCCAGAGGCTGAGGCAAGAGGATTGCTTGAGCCTAGGAGTTTTAGG
CTGCAGTGCCCTATGCATTCCATGCTTGAGCAACACAGGGGGATTCTGTCTAAAATAAA
TAAATCAATAAATAAAAGCAGTGTGTTACTGCAATGAGCATTGTTATATAAATACACAG
TCTTCCACAGAAGTTACAGCACTAGACAGGAAGTTATGGATCTGACTAATTGAGGCTTT
CACCTCTGACTCAGTGTGTGACTCTGGCAAGTGACCTAATGGCTCCAAGCTACAGATTT
TCCAATGGTAAAAGAGAGGAAAACAGGTATCCAACATATTCCACCAGGACATACTGAGA
ATATAATAATAACAATAAATAAATACACATTTTAAGTTCTTGCAATACTTAAGAGGAAA
GGTACTACAAGAAACCAAGATATTTTTCTTAGTGTCACCATAATTTCAGTATCAACAGA
TATGCATTAGGAGCCAAATATTCTAGACATTATGGGATTACAACAGAACAGATGAAAAC
AAATCTCTGCTAGTCTCTGTTTTATAGGCTATTATGGACAAGGTCAGTTTCAGTGGTCA
ACACAGAGCTTATTTAACAGAACATCAAAATGGGGGTGAACGTTAGAGCTCACCTGGAT
TTTATATATATATATATATATATATATATATATATATATATATGTATGAGAGACAGAGA
GAGATCCAAAAGGGGTTAATAATACGGAAACAACTGTCCTCAAAGAAAAGAACCGGCTC
TGGGTTTGAGTCTCAGTGGAAGAGTTTACCATCTGTGCGACCTGGGGCCAGTCACTTAG
CTTTTCCAAGCCAATTTCCTTCCCTCTAAAATAGTGATAGTAACGATCTACTTCAAAGC
GCTCGTGCTTGAAAAACTTTAATCCAGTGGCTGGCTAAGCACCAGAAGTCAACTATTAC
TATTGTTATCGCTGCAGGAGCAAGGTATTTTCTGGCTCTTTCTCTATAAGAAAAACCAC
TGTTTCTCCAGTTAGGCTGCATTCATGAGGCCGAAGCAGAAACCCAAGTGCTTTAAAAA
GCTCGGAGACCGGTGCTGCAGAAACATGAACCCAGTCATCCAGGGCTTTGGTTAAAGCA
CAGCCCCCTCGGCAAAGCCCACCTTTCATTTCCTTCCCTTCCATTTCGGGAAAGCCAAG
CTCCCCCTACGCGTTCGGTTATCTTATTTTCTTGCCTCGCCAGGTCGCTGGCCTGTCTC
TGGCTTCTCTCCGCGACCTCTCGGTCGTGCAGGCTCCGCGGCAGCGAAGCGGCTGGGGC
TGGCGCCTCGCTTCCTCAGCGCTCCATTCTTCCCCTCGGCTCCCGCCGGCCGCAGCCGC
CTTCCGCAGCCGGGGTTCCCGCCGGGATTGACGCGCTGGGGGAGGAGCGGTTTCTCGTT
GCGCGCCTCTAAGGAACATTACGGCAGGGCTCGTTCCTGGCTCCGGCCGCCAGCCCCAG
CCTCCCAGGTCCGGAGCCCGGACTGGCGGAGGCCGCGAGGGAGGGAGCACGAGCGAGGA
GGCACGCGCCCGCCGGTCCGCACCCGGCCCGCCGCAGCCGCCGCCGCCGTCGCCGTCGC
CGCAGCAGCCATGGCCGAGCGCCGCGCCTTCGCCCAGAAGATCAGCAG

B

FIG. 7

```
hCLASP4          ----------------------MFPMEDISISVIGRQRRTVQ----------------- 20
hCLASP5          ----------------------MTHLNSLDVQLAQELG--------------------- 16
hCLASP3          --------------------MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2          ----------------------MLLFPYDDFQTAILRRQGRYICS---------------- 23
hCLASP7          -----------------MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1          MSFRGKVFKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
                                          ..:      .

hCLASP4          --------------------------STVPEDAEKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5          ------------------------------------------------------DFT 19
hCLASP3          N------------------ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2          --------------------------TVPAKAEEEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7          G-----------------------VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1          DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDAEHKAENLLVKEACKFYSSQWHVVNYK 120
                                                                      ::

hCLASP4          YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED--------SSSLCSQKGGVIKQG 105
hCLASP5          DDDLDVVFTPKECRTLQP-SLPEEGVELDPHVR--------------DCVQTYIREWLI 63
hCLASP3          PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR--------------DCIRSYTEDWAI 126
hCLASP2          YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED--------AASLGSQKGGITKHG 107
hCLASP7          ADDLELLLQPRECRTTEP-GIPKD-EKLDAQVR--------------AAVEMYIEDWVI 122
hCLASP1          YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
                  :: .                 :* .  ::* .

hCLASP4          WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5          VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAAQA--GPRHLNVLC 118
hCLASP3          VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMSI 183
hCLASP2          WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7          VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSNDSRRGSGSP 179
hCLASP1          WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSCT 239
                    : :               .::     *    :  :    .   :   .    .

hCLASP4          DVVQCPKMRRHAFELKMLDKYSHYLAAETEQEMEEWLITLKKIIQINTDSLVQEKKETVE 222
hCLASP5          DVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARRTN---------RQAE 169
hCLASP3          DDTPRGSWACSIFDLKNSLPDALLPNLLDRTPNEEIDRQNDDQRKSN---------RHKE 234
hCLASP2          GVVQNNKVRRFAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAAMQEK 219
hCLASP7          EDTPRSSGASSIFDLRNLAADSLLPSLLERAAPEDVDRRNETLRRQH---------RPPA 230
hCLASP1          GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL 299
                            *:*:              .   ::    .   :

hCLASP4          TAQDDETSS----QGKAENIMASLERSMHPELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5          LFALYPSVD----EEDAVEIRPVPECPKEHLG-------N------RILVKLLTLKFEIE 212
hCLASP3          LFALHPSPD----EEEPIERLSVPDIPKEHFG-------------QRLLVKCLSLKFEIE 277
hCLASP2          RNGDSHEDD----EQSKLEGSGSGLDSYLPELAKSAREAEIK---LKSESRVKLFYLDPD 272
hCLASP7          LLTLYPAPD----EDEAVERCSRPEPPREHFG-------------QRILVKCLSLKFEIE 273
hCLASP1          TDLGLDSLDNSVTCECTPEETDSSENNLHADFAKYLTETEDTVKTTRNMERLNLFSLDPD 359
                          .       :                          :   :   : :: :

hCLASP4          VQRLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFNILGQIGDNAKGPPTNVEPFFI 333
hCLASP5          IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARSAVFSV 268
hCLASP3          IEPIFAS----LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2          AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDLSFNLQCCVAENEEGPTTNVEPFFV 327
hCLASP7          IEPIFGI----LALYDVREKKKISENFYFDLNSDSMKGLLRAHGTHPAISTLARSAIFSV 329
hCLASP1          IDTLKLQKKDLLEPESVIKPFEEKAAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
                  : :           .:    : .      : .. :.  :           . :.   * :
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FIG. 8
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```
hCLASP4          NLALFDVKNNCKISADFHVDLNPPSVREMLWGSSTQLASDGSP---KGSSPESYIHGIAE 390
hCLASP5          TYPSSDIYLVVKIEKVLQQGD----IGDCAEPYTVIKESDG------GKSKE-KIEKLKL 317
hCLASP3          TYPSQDVFLVIKLEKVLQQGD----IGECAEPYMIFKEADA------TKNKE-KLEKLKS 382
hCLASP2          TLSLFDIKYNRKISADFHVDLNHFSVRQMLATTSPALMNGS------GQSPSVLKGILHE 381
hCLASP7          TYPSPDIFLVIKLEKVLQQGD----ISECCEPYMVLKEVDT------AKNKE-KLEKLRL 378
hCLASP1          SVALYDLRDSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE 479
                 . .  *:   *:.  :: .    : :          .       .. .   :

hCLASP4          SQLRYIQQGIFSVTNPHPEIFLVARIEKVLQGNITHCAEPYIKNSDPVKTAQKVHRTAKQ 450
hCLASP5          QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVTDVDSVVGRSPVGERRTLA 372
hCLASP3          QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR 437
hCLASP2          AAMQYPKQGIFSVTCPHPDIFLVARIEKVLQGSITHCAEPYMKSSDSSKVAQKVLKNAKQ 441
hCLASP7          AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----SEGERRPAWTDRR 429
hCLASP1          EWLKFPKQAVFSVSNPHSEIVLVAKIEKVLMGNIASGAEPYIKNPDSNKYAQKILKSNRQ 539
                     :  :       :   .  : :      . :

hCLASP4          VCSRLGQYRMPFAWAARPIFKDTQGSLDLDGRFSPLYKQDSSKLSSEDILKLLSEYKKPE 510
hCLASP5          QSRRLSERALSLEENGVGSNFKTS-----TLSVSSFFKQEGDRLSDEDLFKFLADYKRSS 427
hCLASP3          NSSIVGRRSLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLYKFLADMRRPS 496
hCLASP2          ACQRLGQYRMPFAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPE 501
hCLASP7          ---RRGPQ--DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRRPS 483
hCLASP1          FCSKLGKYRRAFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVSDYRRAD 599
                       .                      .: :::*:..::* :*: *:::: ::..

hCLASP4          --KTKLQIIPGQLNITVECVPVDLSNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY 567
hCLASP5          SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPFP-ENRTRPHKEILEFP--TREV 484
hCLASP3          SVLRRLRPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--ARDV 553
hCLASP2          K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH 560
hCLASP7          SLLRRLRPVTAQLKIDISPAPENPHFCLSPELLHIKPYP-DPRGRPTKEILEFP--AREV 540
hCLASP1          R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFIPVKPFNMMAQTEPTVEVEEFVYDSTKY 658
                     ::  : . * : :. ..      :... :  * :           *: **     .

hCLASP4          CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDESDASALKCIYGKPAGSV 627
hCLASP5          YVPHTVYRNLLYVYPQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE 541
hCLASP3          YVPNTTYRNLLYIYPQSLNFAN--RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE 610
hCLASP2          TQPYTIYTNHLYVYPKYLKYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV 620
hCLASP7          YAPHTSYRNLLYVYPHSLNFSS--RQGSVRNLAVRVQYMTG-EDPSQALPVIFGKSSCSE 597
hCLASP1          CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL 718
                 *   * * :*:**  *:: .     ..**::: :::  . *. :..:  *:*:.  .

hCLASP4          FTTNAYAVVSHHNQNPEFYDEIKIELPIHLHQKHHLLFTFYHVSCEINTKGTTKKQDTVE 687
hCLASP5          FLQEVYTAVTYHNKSPDFYEEVKIKLPAKLTVNHHLLFTFYHISCQQ------KQGASVE 595
hCLASP3          FSKEAYTAVVYHNRSPDFHEEIKVKLPATLTDHHHLLFTFYHVSCQQ------KQNTELE 664
hCLASP2          FTRSAFAAVLHHHQNPEFYDEIKIELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVE 680
hCLASP7          FTREAFTPVVYHNKSPEFYEEFKLHLPACVTENHHLLFTFYHVSCQP------RPGTALE 651
hCLASP1          FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHHILFSFYHVTCDINAKANAKKKEALE 778
                 *   .:: * :* :.*:* :*.*:.**   :  :**:*::*:*::*          :   :*

hCLASP4          TPVGFAWVPLLKDGRIITFEQQLPVSANLPPGYLNLNDAESRRQCNVDIKWVDGAKPLLK 747
hCLASP5          TLLGYSWLPILLNERLQTGSYCLPVALEKLPPNYSMHSAEKVPLQNPPIKWAEGHKGVFN 655
hCLASP3          TPVGYTWIPMLQNGRLKTGQFCLPVSLEKPPQAYSVLSPEVP---LPGMKWVDNHKGVFN 721
hCLASP2          TQVGYSWLPLLKDGRVVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGGKPLLK 740
hCLASP7          TPVGFTWIPLLQHGRLRTGPFCLPVSVDQPPPSYSVLTPDVA---LPGMRWVDGHKGVFS 708
hCLASP1          TSVGYAWLPLMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGSDIKWVDGGKPLFK 838
                 * :*::*:*:: . :: :    :*::  .   .   .                ::*.:. * ::.
```

FIG. 8
2 of 6

```
hCLASP4   FKSHLESTIYTQ[illegible]VHKFFHHCQLIQS-------------GSKEV[illegible]LIKYLKCLHAM 794
hCLASP5   IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS 715
hCLASP3   VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS 780
hCLASP2   ISTHLVSTVYTQDQHLHNFFQYCQKTES-------------GAQALGNELVKYLKSLHAM 787
hCLASP7   VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA 767
hCLASP1   VSTFVVSTVNTQDPHVNAFFQECQKREKD-----------MSQSPTSNFIRSCKNLLNVE 887
          ..      *:: .** ::. **   :   :.                :      *.

hCLASP4   EIQVMIQFLPVILMQLFR------------------------VLTNMTH------EDDVP 824
hCLASP5   RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG 775
hCLASP3   QLEPVVRFLHLLLDKLILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG 840
hCLASP2   EGHVMIAFLPTILNQLFR------------------------VLT-RAT------QEEVA 816
hCLASP7   SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVVSLVHRSLEAAQDARG 827
hCLASP1   KIHAIMSFLPIILNQLFK------------------------VLVQNE------EDEIT 916
            . ::  *     :* :*.                       :           .:

hCLASP4   INCTMV-LLHIVSKCHEEGLDS----------YLRSFIKYS-------------FRPEKP 860
hCLASP5   RNCLLASYVHYVFRLPEVQRDVPKSGAPTALLDPRSYHTYGRTSAAAVSSKLLQARVMSS 835
hCLASP3   RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLSN 899
hCLASP2   VNVTRV-IIHVVAQCHEEGLES----------HLRSYVKYA-------------YKAEPY 852
hCLASP7   HCPQLAAYVHYAFRLPGTEPSLPDGAPP----VTVQAATLARGSGRPASLYLARSKSISS 883
hCLASP1   TTVTRV-LPDIVAKCHEEQLDH----------SVQSYIKFV-------------FKTRAC 952
               .   . . :      .                .                 :

hCLASP4   SAPQAQLIH-------ETLATTMIAILKQS------------------------------ 883
hCLASP5   SNPDLAGTHSAADEEVKNIMSSKIADRNCSRMSYYCSGSSDAPSSPA------------- 882
hCLASP3   SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC 959
hCLASP2   VASEYKTVH-------EELTKSMTTILKPS------------------------------ 875
hCLASP7   SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ--------------------------- 915
hCLASP1   KE---RPVH-------EDLAKNVTGLLKSN------------------------------ 972
                          :   .    .

hCLASP4   --------------------ADFLSINKLLKYS-----------------WFFFEIIAKSM 907
hCLASP5   ----------------APRPASKKHFHEELALQ-----------------MVVSTGMVKSM 910
hCLASP3   NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVVCSGSVREsALQQAWFFFELMVKSM 1019
hCLASP2   --------------------ADFLTSNKLLRYS-----------------WFFFDVLIKSM 899
hCLASP7   ------------------WVVSSSAVREAILQHA----------------WFFFQLMVKSM 942
hCLASP1   ---------------------DSPTVKHVLKHS-----------------WFFFAIILKSM 995
                                 .  *                  ..    : ***

                 Cadherin Cleavage
hCLASP4   ATYLLEENKIKLFRGQRFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS 964
hCLASP5   AQHVHNMDKRDSFRRTRFSDRFMDDITTIVNVVTSEIAALLVKPQKENEQAEKMNISLAF 970
hCLASP3   VHHLYFNDKLEAFRKSRFPERFMDDIAALVSTIASDIVSRFQKDTEM---VERLNTSLAF 1076
hCLASP2   AQHLIENSKVKLIRNQRFPASYHHAAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV 956
hCLASP7   ALHLLLGQRLDTFRKLRFPGRFLDDITALVGSVGLEVITRVHKDVEL---AEHLNASLAF 999
hCLASP1   AQHLIDTNKIQLFRPQRFPESYQNELDNLVMVLSDHVIWKYKDALEE---TRRATHSVAR 1052
          . ::    .: .  *  **.  :  .    ::  :  .:     .  .     .. . *:*

hCLASP4   FLKRCLTLMDRGFIFNLINDYISGFSPKDP-----KVLAEYKFEFLQTICNHEHYIPLNL 1019
hCLASP5   FLYDLLSLMDRGFVFNLIRHYCSQLSAKLSNL---PTLISMRLEFLRILCSHEHYLNLNL 1027
hCLASP3   FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRIICSHEHYVTLNL 1136
hCLASP2   FIKRCFTFMDRGFVFKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL 1011
hCLASP7   FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTLNL 1059
hCLASP1   FLKRCFTFMDRGCVFKMVNNYISMFSSGDL-----KTLCQYKFDFLQEVCQHEHFIPLCL 1107
          *:    ::.:*** :*. :.    . .:.       .*    :::* : :*.***:: * *
```

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Cadherin EC motif

```
hCLASP4   PMAFAKPKLQR----------------VQDS--NLEYSLSDEYCKHHFLVGLLLRETSI 1060
hCLASP5   FFMNADTAPTSP--CPSISSQNSSSCSSFQDQKIASMFDLTSEYRQQHFLTGLLFTELAA 1085
hCLASP3   PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFRQQHYLAGLVLTELAV 1196
hCLASP2   PMPFGKGRIQR----------------YQDL--QLDYSLTDEFCRNHFLVGLLLREVGT 1052
hCLASP7   PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGLLLTELAL 1119
hCLASP1   PIRSANIPDPLTP------SES----TQELHASDMPEYSVTNEFCRKHFLIGLLLREVGF 1157
                                    .     :.::  : ::*:* *.:: * .

hCLASP4   ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQLYLPFVGLLLENIQRL 1116
hCLASP5   ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPLVGIILDALP-- 1143
hCLASP3   ILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAMLYLPLIGIIMETVP-- 1254
hCLASP2   ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRI 1108
hCLASP7   ALEPEAEGAFLLHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP-- 1177
hCLASP1   ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI 1213
           *:        ::  .:  ::.*:  *  * *      :.::* **:*: .:  : :

hCLASP4   AGRDTLYSCA----------AMPN-S----ASRDEFPCGFTSPANRGSLSTDKDTAYGS 1160
hCLASP5   ----------------------QL---------------CDFTVADTRRYRTSGSD----- 1162
hCLASP3   ----------------------QLY---------------DFTETHNQRGRPICIATDD-- 1276
hCLASP2   NVRDVSPFPVNAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167
hCLASP7   ----------------------RLH---------------DFAEGPGQRSRLASMLDSDTE 1201
hCLASP1   YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSKDVLNSIAAFSSIAIS 1273
                                                  . :

hCLASP4   FQ-NGHGIKREDSRGSLIPEGATGFPDQGNTGEN------TRQSSTRSSVSQYNRLDQYE 1213
hCLASP5   ---------EEQEGAGAINQNVALAIAGNNFNLKT------SGIVLSSLPYKQYNMLNADT 1208
hCLASP3   ---------YESESGSMISQTVAMAIAGTSVPQLTR----PGSFLLTSTSGRQHTTFSAES 1324
hCLASP2   STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSE 1227
hCLASP7   ---------GEGDIAGTINPSVAMAIAGGPLAPGSR----ASISQGPPTASRAGCALSAES 1249
hCLASP1   ------TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327
                     . :  . :    :          .                .     :.

hCLASP4   IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFRYMGKRNIARVHDA 1273
hCLASP5   TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ 1268
hCLASP3   SRSLLICLLWVLKNADETVLQKWFTDLSVLQLNRLLDLLYLCVSCFEYKGKKVFERMNSL 1384
hCLASP2   IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEG 1287
hCLASP7   SRTLLACVLWVLKNTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKAFERINSL 1309
hCLASP1   TRSLLMCFLHIMKTISYETLIAYWQRAPSPEVSDFFSILDVCLQNFRYLGKRNIIRKIAA 1387
           :.*: * * ::*  .  :  :    .  ::  :: :  :*:  *.* **:   :

hCLASP4   WLSKHFGIDR----------------KSQTMPALRNRSGVMQARLQHLSSLESS------ 1311
hCLASP5   VLQKSRDVKAR----------------LEEALLRGEGARGEMMRRRAPGNDRFPGLNEN--- 1311
hCLASP3   TFKKSKDMRAK----------------LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430
hCLASP2   LGPIVHDRKS----------------QTLPVSRNRTGMMHARLQQLGSLDNS------ 1323
hCLASP7   TFKKSLDMKAR----------------LEEAILGTIGARQEMVRRSRERSPFGNPEN----- 1350
hCLASP1   AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSQTLPIIRGKN----- 1442
                 .                          :    :    :

hCLASP4   ------------FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFKTQLL 1359
hCLASP5   --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368
hCLASP3   ENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489
hCLASP2   ------------LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7   --VRWRKSVTHWKQTSDRVDKTKDEMEHEALVEGNLATEASLVVLDTLEIIVQTVM-LSE 1407
hCLASP1   --ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDLVSLFTQTHQRQLQ 1500
                        .     .  :: :.    ..* *** *  **  . .
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hCLASP4     NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY 1419
hCLASP5     CKDS---LLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIAKFGDLLFEEEVEQCFDLCH 1425
hCLASP3     SKES---ILGGVLKVLLHSMACNQSAVYLQHCFATQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2     ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431
hCLASP7     ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464
hCLASP1     QCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
                  .    ::   :   :  :   **   * : ::: * :: ** . :::  .: *  :*

hCLASP4     EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5     QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3     RLLRHCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2     EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7     RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1     EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
            .:*: *       :....  **::**   .:    .: * ::*:  :::.*:.     .

hCLASP4     SRFQESLFIINNFANSDRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539
hCLASP5     EHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3     EFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILSDTVKMKEHQEDPEMLIDLM 1664
hCLASP2     TRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7     EHLRRSLKTILTYAEEDMGLRDSTFAEQVQDLMFNLHMILTDTVKMKEHQEDPEMLIDLM 1582
hCLASP1     SRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679
              ::.**      :: *  :: : *. :*::*  .:. :*  *.:*:*.::***** :**
                                                transmembrane
hCLASP4     YSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHVAALVAEFLHRKK------- 1592
hCLASP5     YRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3     YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLEDR----- 1718
hCLASP2     YSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRKG------- 1604
hCLASP7     YRIARGYQGSPDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLALLEDQ----- 1637
hCLASP1     YSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHIAALIAEYLKRKGYWKVEKI 1739
            * :*..*  :*: * ***:.**  * .    :*** * :* :**:**:*

hCLASP4     ----------------------------LFPNGCSAFKKITPNIDEEGAMKEDAGMMD---- 1622
hCLASP5     ----------------------------SYLPVGSVSFQNISSNVLEESVVSEDTLSPDEDGV 1633
hCLASP3     ----------------------------KYLPVGCVTFQNISSNVLEESAVSDDVVSPDEEGI 1753
hCLASP2     ----------------------------VFRQGCTAFRVITPNIDEEASMMEDVGMQD---- 1634
hCLASP7     ----------------------------RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1     CTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPNIKEEGAAKEDSGMHD---- 1795
                                       :  *  :*  *:.*: **.   :*    *
                                                                 ITAM
hCLASP4     ---VHYSEEVLLELLEQCVDGLWKAERYEIISEISKLIVPIYEKRREFEKLTQVYRTLHG 1679
hCLASP5     CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3     CSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPIHEANRDAKKLSTIHGKLQE 1813
hCLASP2     ---VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRR---------------- 1677
hCLASP7     CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAAVHGKLQE 1732
hCLASP1     ---TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAVFEKQRDFKKLSDLYYDIHR 1852
                 :.*  *:  *   .   :   .  ** : :: * ::.: * .*
            ITAM                DOCK motif      DOCK motif                ITAM
hCLASP4     AYTKILEVMHTKKRLLGTFFRVAFYGQSFFEEEDGKEYIYKEFKLTGLSEISLRLVKIYG 1739
hCLASP5     AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFVYKEFAITKLPEISHRLEAFYG 1750
hCLASP3     AFSKIVHQSTGWERMFGTYFRVGFYG-TKFGDLDEQEFVYKEFAITKLAEISHRLEGFYG 1872
hCLASP2     ----------------------------DFFEDEDGKEYIYKEFKLTPLSEISQRLLKIYS 1710
hCLASP7     AFTKIMHQSSGWERVFGTYFRVGFYG-AHFGDLDEQEFVYKEFSITKLAEISHRLEEFYT 1791
hCLASP1     SYLKVAEVVNSEKRLFGRYYRVAFYGQGFFEEEEGKEYIYKEFKLTGLSEISQRLLKIYA 1912
                                      * : :  :*:::**** :* *.*** **   :*
```

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                 ITAM                                  ITAM
hCLASP4          EKFGTENVKIIQDSDKVNAKELDPHYAHIQVTYVKEYFDDKELTERKTEFERNHNISRFV 1799
hCLASP5          QCFGAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEEYFDEYEMKDRVTYFEKNFNLRRFM 1810
hCLASP3          ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEEYFDTYEMKDRITYFDKNYNLRRFM 1932
hCLASP2          DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRRFM 1770
hCLASP7          ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQITYVEEYFDTYELKDRVTYFDRNYGLRTFL 1851
hCLASP1          DKFGADNVKIIQDSNKVNPKDLDPKYAYIQVTYVTEFFEEKEIEDRKTDFEMHHNINRFV 1972
                 : ** : *::*:**   *:   .**.: *:**:*.* *:*:  *: :* * *:  ..:  *:
                                                        ITAM              DOCK motif
hCLASP4          FEAPYTLSGKKQGCIEEQCKRRTILTTSNSFPYVKKRIPINCEQQINLKPIDGATDEIKD 1859
hCLASP5          YTTPFTLEGRPRGELHEQYRRNTVLTTMHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKK 1870
hCLASP3          YCTPFTLDGRAHGELHEQFKRKTILTTSHAFPYIKTRVNVTHKEEIILTPIEVAIEDMQK 1992
hCLASP2          FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSK 1830
hCLASP7          FCTPFTPDGRAHGELPEQHKRKTLLSTDHAFPYIKTRIRVCHREETVLTPVEVAIEDMQK 1911
hCLASP1          FETPFTLSGKKHGGVAEQCKRRTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSR 2032
                 :   *:*  *: :* : ** :*.*:*:: : ***:*.*: :   .   *.*:: *  :::.
                      Coiled-coil
hCLASP4          KTAELQKLCSSTDVDMIQLQLKLQQWVSVQVNAGPLAYARAFLNDSQASKYPPKKVSELK 1919
hCLASP5          KTLQLAVAINQEPPDAKMLQMVLQQSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKLR 1930
hCLASP3          KTQELAFATHQDPADPKMLQMVLQQSVGTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLR 2052
hCLASP2          KVAELRQLCSSAEVDMIKLQLKLQQSVSVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLK 1890
hCLASP7          KTRELAFATEQDPPDAKMLQMVLQQSVGPTVNQGPLEVAQVFLAEIPEDPKLFRHHNKLR 1971
hCLASP1          KVSELNQLCTMEEVDMISLQLKLQQSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK 2092
                 *. :*          *    **: *** *.  ** **:  *:.** :   .    .: . *:
                                                Coiled-coil
hCLASP4          DMFRKFIQACSIALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIHEQILQEDTMHSP 1979
hCLASP5          LCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENLRPMIERKIPELYKPIFR 1990
hCLASP3          LCFKDFTKRCEDALRKNKSLIGPVQKEYQRELGKLSSP---------------------- 2090
hCLASP2          EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS- 1949
hCLASP7          LCFKDFCKKCEDALRKNKALIGPDQKEYHRELERNYCRLREALQPLLTQRLPQLMAPTP- 2030
hCLASP1          EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMLSELSTVMNEQITGRDDLSKR 2152
                   *:.*     * *:   *: **    * **:. :
                                                   PDZ ligand
hCLASP4          WMSNTLHVFCAISGTSSDRGYGSPHYAEV-- 2008
hCLASP5          VESQKRDSFHRSSFRKCETQLSQGS------ 2015
hCLASP3          -------------------------------
hCLASP2          VLPNSLHIFNAISGTPTSTMVHGMTSSSSVV 1980
hCLASP7          --PGLRNSLNRASFRKADL------------ 2047
hCLASP1          GVDQTCTRVISKATPALPTVSISSSAEV--- 2180
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FIG. 8
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